

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 2, 2001, 18:17:06 ; Search time 15.93 Seconds

(Without alignments)
1841.005 Million cell updates/sec

Title: US-09-402-845-2

Perfect score: 2060

Sequence: 1 MGAVPLPLSPRTASLSIGFL.....DMATECMATSSHQIVGALG 385

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1818	88.3	381	2 JH0152	acid phosphatase (
2	1661.5	80.7	386	1 JH0610	acid phosphatase (
3	1022.5	49.6	423	1 S06167	acid phosphatase (
4	1020.5	49.5	421	2 S14742	acid phosphatase (
5	1019.5	49.5	423	2 A33395	acid phosphatase (
6	617	30.0	438	2 S64682	acid phosphatase (
7	487	23.6	440	2 T32457	hypothetical prote
8	480	23.3	366	2 T25060	hypothetical prote
9	479	23.3	376	2 T24223	hypothetical prote
10	375	18.2	449	2 T15933	hypothetical prote
11	329	16.0	452	2 T20556	hypothetical prote
12	310	15.0	755	2 T19118	hypothetical prote
13	287.5	14.0	380	2 T16883	hypothetical prote
14	274	13.3	413	2 T18945	hypothetical prote
15	271.5	13.2	416	2 T16058	hypothetical prote
16	250.5	12.2	408	2 T20893	hypothetical prote
17	247.5	12.0	471	2 T18944	hypothetical prote
18	220	10.7	462	2 T40420	probable acid phos
19	189.5	9.2	523	2 T15649	hypothetical prote
20	180.5	8.6	391	2 T27918	hypothetical prote
21	169	8.2	465	2 A86233	histidine acid pho
22	167.5	8.1	465	2 JEO369	hypothetical prote
23	158	7.7	969	2 T27997	hypothetical prote
24	144.5	7.0	701	2 T20892	hypothetical prote
25	143.5	7.0	537	2 S54770	secreted acid phos
26	143.5	7.0	888	2 T46726	secreted acid phos
27	134.5	6.5	251	2 T46373	hypothetical prote
28	129.5	6.3	463	2 T39929	thiamin-repressibl
29	129	6.3	413	2 B85636	periplasmic glucos

30	121	5.9	413	2 JVO087	glucose-1-phosphat
31	115.5	5.6	737	2 T30795	hypothetical prote
32	115.5	5.6	737	2 F42508	E2L protein - vacc
33	112.5	5.5	737	2 A72156	C2L protein - vari
34	110	5.3	599	1 RRBPM	RNA-directed RNA p
35	109.5	5.3	737	2 E36841	E2L protein - vari
36	108.5	5.3	737	2 T28481	hypothetical prote
37	106	5.1	463	2 S14119	acid phosphatase (
38	105	5.1	417	2 S25627	glucose-1-phosphat
39	104.5	5.1	432	2 B36733	acid phosphatase (
40	104	5.0	489	1 RBBYP4	PERT494 protein pre
41	104	5.0	597	2 A35928	hypothetical 86k p
42	102.5	5.0	479	1 JN0890	acid phosphatase (
43	102	5.0	444	2 D85633	hypothetical prote
44	101	4.9	801	2 T14338	sucrose synthase (
45	99	4.8	899	2 T11578	probable lipoxigen

ALIGNMENTS

RESULT 1

JH0152
acid phosphatase (EC 3.1.3.2) precursor, prostatic - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999

C:Accession: JH0152; S41252

R:Roiko, K.; Jaenne, O.A.; Vilho, P.

Gene 89, 223-229, 1990

A:Title: Primary structure of rat secretory acid phosphatase and comparison to other

A:Reference number: JH0152; MUID:90323620

A:Accession: JH0152

A:Molecule type: mRNA

A:Residues: 1-381 <ROI>

A:Cross-references: GB:M32397; NID:q206028; PIDN:AAA41806.1; PID:q206029

R:Virkkunen, P.H.; Hedberg, P.; Palvimo, J.J.; Birr, E.; Porvari, K.; Taavitsainen, P

submitted to the EMBL Data Library, September 1993

A:Description: Structural organization of human and rat prostate-specific acid phosph

sequence in the human gene promoter.

A:Reference number: S41251

A:Accession: S41252

A:Molecule type: DNA

A:Residues: 1-39 <VIR>

A:Cross-references: EMBL:X74969; NID:q439674; PIDN:CAA52914.1; PID:q439675

C:Superfamily: mammalian acid phosphatase

C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-381/Product: acid phosphatase, prostatic #status predicted <MAT>

F:42/Active site: Arg #status predicted

F:43/Active site: His (phosphohistidine intermediate) #status predicted

F:93-219,332/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.3% Score 1818; DB 2; Length 381;

Best Local Similarity 88.5%; Pred. No. 5.4e-139;

Matches 337; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY	1	MGAVPLPLSPRTASLSIGFL	LDLPGQAKELFTLVFRH	DGRPIETFPDPTRES	60
DB	1	MRAPVHLVGTASLTGLFL	LLSLRDPGQAKELFTLV	FRHGRPIETFPDPTRES	60
QY	61	SWPGFQQLTQWGEQHYEL	SYTRKRGRLNTYKHQDI	YIYSTVDRLMAMNTLA	120
DB	61	SWPGFQQLTQWGEQHYEL	SYTRKRGRLNTYKHQDI	YIYSTVDRLMAMNTLA	120
QY	121	ALPPEGISINWPRLLMOP	IVHTVLSIEDRLTLVPR	DCRFPELSETESEFRL	180
DB	121	ALPPEGISINWPRLLMOP	IVHTVLSIEDRLTLVPR	DCRFPELSETESEFRL	180
QY	181	HPYKSLDTLSSLSGFDOD	LFGLMSKVDPLFCESV	HNFTLPMSWATEDAMIK	240
DB	181	QPYKSLDTLTPSLSGFDOD	LFGLMSKVDPLFCESV	HNFTLPMSWATEDAMIK	240

QY 241 SLSTLYGHHKQEKSRLOGGLVNLNKLATOPQKYYKVLWYSADHTTVSGLOMALD 300
 :|||||
 Db 241 SLSTLYGHHKQEKSRLOGGLVNLNKLATOPQKYYKVLWYSADHTTVSGLOMALD 300
 :|||||
 QY 301 VYNGVLPPYASCHMMLKLVHDKGHHFVEMVYRNENQNEPYLTLTQCTHSCPLEKFAELLD 360
 :|||||
 Db 301 LNYGLLPPYASCHMMLKLVHDKGHHFVEMVYRNENQNEPYLTLTQCTHSCPLEKFAELLD 360
 :|||||
 QY 361 PVIPQDMATECMATSSHOGTV 381
 :|||||
 Db 361 PVIPQDMATECMATSSHOGTV 381
 :|||||
 RESULT 2
 JH0610
 acid phosphatase (EC 3.1.3.2) ACP precursor [valinated] - human
 N:Alternate names: acid phosphatase, prostatic; orthophosphoric monoester phosphohydrolyase
 C:Species: Homo sapiens (man)
 C:Date: 17-Aug-1992 #sequence_revision 01-Dec-1995 #text_change 08-Dec-2000
 C:Accession: JH0610; J50593; A38608; S0131; A32419; S1147; S38863; S41251; S17042; S4242
 R:Shier, F.S.; Li, S.S.L.
 Biochem. Biophys. Res. Commun. 184, 1468-1476, 1992
 A>Title: Structure of human prostatic acid phosphatase gene.
 A:Reference number: JH0610; MUID:92272747
 A:Accession: JH0610
 A:Molecule type: DNA
 A:Residues: 1-386 <SHN>
 A:Cross-references: GB:M97580; GB:M97581; GB:M97582; GB:M97583; GB:M97584; GB:M97585; GB:M97586
 A:Accession: J50593
 A:Molecule type: mRNA
 A:Residues: 1-386 <SH>
 A:Cross-references: GB:M97589; NID:g189611; PIDN:AAA60021.1; PID:g189613
 R:Van Etten, R.L.; Davidson, R.; Stevis, P.E.; MacArthur, H.; Moore, D.L.
 J. Biol. Chem. 266, 2313-2319, 1991
 A>Title: Covalent structure, disulfide bonding, and identification of reactive surface
 A:Reference number: A38608; MUID:91115848
 A:Accession: A38608
 A:Molecule type: mRNA
 A:Residues: 1-386 <VAN>
 A:Cross-references: GB:M34840; NID:g189620; PIDN:AAA69694.1; PID:g189621
 A>Note: part of this sequence, including the amino end of the mature protein, was confirmed
 R:Vilho, P.; Viikonen, P.; Henttu, P.; Kolko, K.; Solin, T.; Hultala, M.L.
 FEBS Lett. 236, 275-281, 1988
 A>Title: Molecular cloning and sequence analysis of cDNA encoding human prostatic acid phosphatase
 A:Reference number: S01331; MUID:88312981
 A:Accession: S01331
 A:Molecule type: mRNA
 A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-65, 'WHPPTHPA', 74-211, 'A', 213-386 <VH>
 A:Cross-references: EMBL:X52174; NID:928321; PIDN:CAA34422.1; PID:g28322
 A>Note: part of this sequence, including the amino end of the mature protein, was confirmed
 R:Shier, F.S.; Lee, H.; Leidenman, M.M.; Lundwall, A.; Deaven, L.L.; Lee, C.; Li, S.S.
 Biochem. Biophys. Res. Commun. 160, 79-86, 1989
 A>Title: Human prostatic acid phosphatase: cDNA cloning, gene mapping and protein sequencing
 A:Reference number: A32419; MUID:85228054
 A:Accession: A32419
 A:Molecule type: mRNA
 A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-94, 'D', 96-115, 'R', 117-214, 'S', 216-293, 'T', 295-386 <VH>
 A:Cross-references: GB:M4902; NID:g189618; PIDN:AAA60022.1; PID:g189619
 A>Note: the authors translated the codons GAC for residue 95 as Glu, CGT for residue 116 as Arg, and CAA for residue 117 as Gln.
 R:Talbot, P.G.; Govindan, M.V.; Patel, P.C.
 Nucleic Acids Res. 18, 4928, 1990
 A>Title: Nucleotide sequence of human prostatic acid phosphatase determined from a full-length cDNA
 A:Reference number: S1147; MUID:90370491
 A:Accession: S1147
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'R', 67-138, 'E', 140-156, 'R', 158-214, 'S', 216-293, 'T', 295-386 <VH>
 A:Cross-references: EMBL:X53605; NID:g35683; PIDN:CAA37673.1; PID:g35684
 R:Baner, B.; Blaschke, D.; Fittler, F.; Hoer, W.
 submitted to the EMBL Data Library, April 1993
 A:Description: Characterization of the promoter of the human prostatic acid phosphatase
 A:Reference number: S38863
 A:Accession: S38863

A: Molecule type: DNA
A: Residues: 1-40 <BAN>
A: Cross-references: EMBL:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531
R.Virkkunen, P.H.; Hedberg, P.; Palvimo, J.J.; Birt, E.; Porvari, K.; Taavitsaaten, P.
Submitted to the EMBL Data Library, September 1993
A: Description: Structural organization of human and rat prostate-specific acid phosphatase in the human gene promoter.
A: Reference number: S41251
A: Accession: S41251
A: Molecule type: DNA
A: Residues: 1-40 <VIR>
A: Cross-references: EMBL:X74961; NID:9439657; PIDN:CAA52913.1; PID:9439658
R.Lee, H.; Chu, T.M.; Li, S.S.L.; Lee, C.
Biochem. J. 277, 759-765, 1991
A: Title: Homodimer and heterodimer subunits of human prostate acid phosphatase.
A: Reference number: S17042; MUID:91336999
A: Accession: S17042
A: Status: preliminary
A: Molecule type: protein
A: Residues: 33-49 <LEE>
R.Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.
Biochim. Biophys. Acta 1217, 188-194, 1994
A: Title: Analysis of the promoter of the human prostatic acid phosphatase gene.
A: Reference number: S42730; MUID:9415395
A: Accession: S42730
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-40 <BA2>
A: Cross-references: GB:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531
R.Sharief, F.S.; Li, S.S.
Biochem. Mol. Biol. Int. 33, 561-565, 1994
A: Title: Nucleotide sequence of human prostatic acid phosphatase ACP gene.
A: Reference number: I37175; MUID:95038536
A: Accession: I37175
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-386 <RES>
A: Cross-references: EMBL:U07097; NID:9515995; PIDN:AA60640.1; PID:9515997
C: Comment: This protein is synthesized under androgen regulation by epithelial cells
C: Genetics:
A: Gene: GDB:ACPP
A: Cross-references: GDB:119644; OMIM:171790
A: Map position: 3q21.3-3q25.2
A: Introns: 40/3; 72/3; 101/3; 152/3; 185/3; 216/3; 260/3; 288/3; 323/2
C: Function:
A: Description: catalyzes the hydrolysis of a wide range of phosphate esters
C: Superfamily: mammalian acid phosphatase
C: Key words: glycoprotein; phosphonitridine; phosphoprotein; phosphoric monoester hydr
F.1-32/doman; signal sequence #status predicted <SIG>
F.33-386/Product: acid phosphatase ACP #status experimental <MAT>
F.43, 86/Active site: Arg #status predicted
F.44/Active site: His (phosphonitridine intermediate) #status predicted
F.94, 220, 333/Binding site: carboxylate (Asn) (covalent) #status experimental
F.161-372, 215-313, 347-351/Disulfide bonds: #status experimental

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||||| : || ||| ||||||||| : ||||||||| ||||||| : |||
Db 181 LHPKDFIATIGKISGLHGDLFCIWSKVYDPLCESEHNHTLPSWATEDMTLRELSE 240
OY 240 LSLSLVGIHKOKKSRLOGGVNLVETILKNKLATOPQKYKLVMSAHDITVSGLOMAL 299
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 241 LSLSLVGIHKOKKSRLOGGVNLVETILKNKLATOPQKYKLVMSAHDITVSGLOMAL 300
OY 300 DVNNGVLPYASCHMMLYHDKGHFVEMRYRNFTONEPRLTLPCTHSCPLEKFAELL 359
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 301 DVNNGVLPYASCHMMLYHDKGHFVEMRYRNFTONEPRLTLPCTHSCPLEKFAELL 360
OY 360 DVNNGVLPYASCHMMLYHDKGHFVEMRYRNFTONEPRLTLPCTHSCPLEKFAELL 360
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 361 GVPVLPQDMSTECMTNTHGCT 381

RESULT 3
S06167
acid phosphatase (EC 3.1.3.2) ACP2 precursor [validated] - human
N:Alternate names: acid phosphatase, lysosomal
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1992 #sequence_revision 01-Dec-1995 #text_change 08-Dec-2000
C:Accession: S06167; S05525; S01155
R: von Figura, K.
Submitted to the EMBL Data Library, June 1989
A:Reference number: S06167
A:Accession: S06167
A:Molecule type: DNA
A:Residues: 1-423 <VON>
A:Cross-references: EMBL:X15525; NID:934239; PIDN:CAA3542.1; PID:91199524
R: Geier, C.; von Figura, K.; Pohlmann, R.
Eur. J. Biochem. 183, 611-616, 1989
A:Title: Structure of the human lysosomal acid phosphatase gene.
A:Reference number: S05525; MUID:89377828
A:Accession: S05525
A:Molecule type: DNA
A:Residues: 1-29 <GEI>
R: Pohlmann, R.; Krentler, C.; Schmidt, B.; Schroeder, W.; Lorkowski, G.; Culley, J.; Merz
EMBO J. 7, 2333-2350, 1988
A:Title: Human lysosomal acid phosphatase: cloning, expression and chromosomal assignment
A:Reference number: S01155; MUID:89052645
A:Accession: S01155
A:Molecule type: mRNA
A:Residues: 1-423 <POH>
A:Cross-references: EMBL:X12548; NID:934262; PIDN:CAA31064.1; PID:934263
A:Note: Part of this sequence, including the amino end of the mature protein, was confir
C:Genetics:
A:Gene: GDB:ACP2
A:Cross-references: GDB:118963; OMIM:171650
A:Map position: 11p11.2-11p11.11
A:Insertions: 38/3; 70/3; 99/3; 150/3; 183/3; 213/3; 258/1; 285/3; 321/2; 380/1
C:Function:
A:Description: catalyzes the hydrolysis of a wide range of phosphate esters
C:Superfamily: mammalian acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydroly
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-423/Product: acid phosphatase ACP2 #status experimental <MAP>
F:41/Active site: Arg #status predicted
F:42/Active site: His (phosphohistidine intermediate) #status predicted
F:92,133,167,177,191,267,322,331/Binding site: carboxylate (Asn) (covalent) #status pre
F:159-370,212-310,345-349/Dissulfide bonds: #status predicted

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Query Match 49.5%; Score 1020.5; DB 2; Length 421;
Best Local Similarity 51.4%; Pred. No. 9.3e-74;
Matches 187; Conservative 66; Mismatches 106; Indels 5; Gaps 3;

Db 73 MLOHWELOALRQRYHGFPLNTSYHROEVYVRSJFDRTLMSAEANLAGLPPNMGQRFNP 132
OY 134 RLMOPIPVHTVSLSEDRLLYLPRDCPRFEELKSETLSEEFKLRLHPYKSLDTLSL 193
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 133 NISQPIPVHTVPTEDRLKLFPLGCPRYEQLOLNETRQRPYONESSRNAQFIDMVA NE 192
OY 194 SCFDDODLFGIWSKVYDPLCESEHNHTLPSWATEDMTLRELSE 240
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 193 TGLTDLTLETVMN-VYDTLFCEDQTHGLRLPPWASPOQTMRLSRUKDFSFRFLFGIYQDAE 251
OY 254 KSRLQGVNLVETILKNKLATOPQKYKLVMSAHDITVSGLOMALDVNNGVLPYASCH 313
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 252 KARLQGVNLVETILKNKLATOPQKYKLVMSAHDITVSGLOMALDVNNGVLPYASCH 311
OY 314 MMELYHDKGHF-VEMRYRNFTONEPRLTLPCTHSCPLEKFAELLDPVLPQDMATECM 372
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 312 IFELYQEDSGNFSEVMEYRNESDKAPWPLSPGCPHRCPLDPLRLTEPVVPKDMQOECQ 371
OY 373 ATSSHOGT 380
Db 372 LASGPADT 379

RESULT 4
S14742
acid phosphatase (EC 3.1.3.2) precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Mar-2000
C:Accession: S14742
R: Geier, C.; von Figura, K.; Pohlmann, R.
Biochem. Hoppe-Seyler 372, 301-304, 1991
A:Title: Molecular cloning of the mouse lysosomal acid phosphatase.
A:Reference number: S14742; MUID:91282986
A:Accession: S14742
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-421 <GEI>
A:Cross-references: EMBL:X57199; NID:952870; PIDN:CAA0485.1; PID:952871
C:Superfamily: mammalian acid phosphatase
C:Keywords: lysosome; phosphoric monoester hydrolase

Query Match 49.5%; Score 1020.5; DB 2; Length 421;
Best Local Similarity 51.4%; Pred. No. 1.3e-74;
Matches 187; Conservative 66; Mismatches 106; Indels 5; Gaps 3;

Db 21 LLSLCL--DPGQAKELKFTLVFRHGDGRPIETFPDPTRESSWPGFQGLTQWGMEOH 77
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 15 LLSLCLVMPPIQARSLRFVTILYRHGDRSPVKTYPDPOEKKWPGFQGLTQWGMEOH 74
OY 78 YELGSYTRKRYGRPLNDYKHKDQIYIRSTVDRTLMSAMTNLAALPPEGISITWNPRLTW 137
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 75 WELQOALRQRYHGFPLNTSYHROEVYVRSJFDRTLMSAEANLAGLPPNEVQHFSPNLSW 134
OY 138 QPITVHVVSLEDRLLYLPRDCPRFEELKSETLSEEFKLRLHPYKSLDTLSLSCGFD 197
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 135 QPITVHVVSLEDRLLYLPRDCPRFEELKSETLSEEFKLRLHPYKSLDTLSLSCGFD 194
OY 198 DODLFGIWSKVYDPLCESEHNHTLPSWATEDMTLRELSE 240
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 195 NVTLTETVMN-VYDTLFCEDQTHGLRLPPWASPOQTMRLSRUKDFSFRFLFGIYQDAE 253
OY 258 QGVNLVETILKNKLATOPQKYKLVMSAHDITVSGLOMALDVNNGVLPYASCHMML 317
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 254 QGVNLVETILKNKLATOPQKYKLVMSAHDITVSGLOMALDVNNGVLPYASCHMML 313
OY 318 YHDKGHP-VEMRYRNFTONEPRLTLPCTHSCPLEKFAELLDPVLPQDMATECMATSS 376
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 314 YQEDNGNFSVMEYRNESDKAPWPLSPGCPHRCPLDPLRLTEPVVPKDMQOECQ 373
OY 377 HOGT 380
Db 374 TADT 377

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DR N-PSDB: AAV45592.
XX New mouse prostatic acid phosphatase - used to induce an immune
PT response against tumour related antigens
XX
PS Claim 1; Page 20-21; 30pp; English.
XX
CC This is the amino acid sequence of mouse prostatic acid phosphatase
CC (PAP), a novel tumour associated antigen. PAP cDNA (see AAV45592)
CC was cloned from mouse prostate organ cDNA, and can be used in the
CC recombinant production of mouse PAP. A method for producing an
CC immune response against an autologous polypeptide tumour antigen
CC (e.g. human PAP) involves immunising a subject with a xenogeneic
CC antigen (e.g. mouse PAP), either alone, as part of a viral antigen
CC construct, or as part of a pulsed dendritic cell preparation.
CC Recombinant viruses expressing PAP are used in compositions to
CC elicit immune responses against a tumour related antigen. The
CC compositions are also useful for reducing tumour cell load.
XX
SQ Sequence 385 AA;

Query Match 100.0%; Score 2060; DB 20; Length 385;
Best Local Similarity 100.0%; Pred. No. 5e-196;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAVPLPLSPYASLSIGFLLLSCLDPGQAKELKFTLVFRHGRGPIETFPDPTES 60
DB 1 mgavplplspyaalslsgfllllscldpqgakekftlvfrhgrgrliefpdples 60
QY 61 SSWPGFQGLTQWGMEOHVEGYSYRKRGRFLNDTYKHDQIYIRSTVDRTLMSAMTILA 120
DB 61 swpgfsglqtqwgmeqhyelgsytrkrygrflndtykhdqiyirstvdrtlmsamtla 120
QY 121 ALFPEEGISINNPRLMQPIPVHTVSLSEDRLLYLPFDCRPREELKSETLSEEFLLKRL 180
DB 121 alfppegislnnprrlmqpipvhtvslsedrlllylpfdrpreelkseetleesefllkrl 180
QY 181 HPYKSFLLDTLSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPSWATEDAMIKELSEL 240
DB 181 hpyksflldtlsslsgfdqdlfglmskvydplfcesvhnftlpswatedamikelssel 240
QY 241 SLSLSYGIHKKKESRLOGGVLVNEILKNMKLATOPQKYLWYSANDTIVSGIOMALD 300
DB 241 slslsygihkksrloggvlnelknmklatqpkykklwysandtvtsglqmal 300
QY 301 VYNGVLPYASCHMMELCYHDKGFVEMYRNETQNEPYPLTLPGCTHSCPLEKFAELL 360
DB 301 vyngvlpypaschmmelyhdkgfhvemyrnetqnepypltlpgcthsoplekfaell 360
QY 361 PVIPQDWATECMATSSHQGTGALG 385
DB 361 pvipqdwatecmatsshggtvgalg 385

RESULT 2
AAW57418 standard; Protein: 386 AA.
XX
AC AAW57418;
XX
DT 07-AUG-1998 (first entry)
XX
DE Protein encoded by a human prostate cancer marker.
XX
KM Prostate cancer; human; marker; diagnosis; treatment; probe.
XX
OS Homo sapiens.
XX
PN WO9804689-A1.
XX
PD 05-FEB-1998.
XX

PF 31-JUL-1996; 96WO-US12516.
XX
PR 31-JUL-1996; 96WO-US12516.
XX
PA (UROC-) UROCOR INC.
XX
PI An G, O'hara SM, Ralph D, Veltri R;
DR WPI: 1998-130681/12.
XX
DR N-PSDB: AAV29653.
XX
PT Human prostate cancer marker - useful for detection and treatment of
PT human prostate cancer
XX
PS Disclosure; Pages 167-174; 229pp; English.
XX
CC This protein is encoded by a marker sequence for human prostate cancer.
CC Isolated nucleic acid segments shown in AAV16881 to AAV16885, AAV16890
CC to AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer
CC markers are provided in the specification. It also provides methods for
CC identifying markers for human prostate cancer and for detection of
CC prostate cancer cells. The markers can be identified by amplifying human
CC prostate RNA to provide nucleic acid amplification products, separating
CC the products and identifying those RNA that are differentially expressed
CC between human prostate cancers versus normal or benign human prostate.
CC prostate cancer cells in a sample can be detected by detecting a nucleic
CC acid in a sample, the nucleic acid being a prostate cancer marker.
CC probes and primers derived from this marker can be used for the detection
CC of prostate cancer cells in a sample. Antibodies against the protein
CC encoded by the marker nucleic acid fragments, inhibitors of the protein
CC and oligonucleotides antisense to the markers can be used in the
CC treatment of prostate cancer. The antibodies can also be used for the
CC diagnosis of human prostate cancer.
XX
SQ Sequence 386 AA;

Query Match 80.7%; Score 1661.5; DB 19; Length 386;
Best Local Similarity 81.6%; Pred. No. 1.9e-156;
Matches 311; Conservative 26; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAVPLPLSPYASLSIGFLLLSCLDPG-QAKELKFTLVFRHGRGPIETFPDPTTE 59
DB 1 mraeplllraaaslsigfllflfwldrtsvlakelkftlvfrhgrdrtspidrtfpdpke 60
QY 60 SSWPGFQGLTQWGMEOHVEGYSYRKRGRFLNDTYKHDQIYIRSTVDRTLMSAMTIL 119
DB 61 swpgfsglqtqwgmeqhyelgsytrkrygrflndtykhdqiyirstvdrtlmsamtln 120
QY 120 AALFPEEGISINNPRLMQPIPVHTVSLSEDRLLYLPFDCRPREELKSETLSEEFLLK 179
DB 121 aalfpegvislnnprrlmqpipvhtvslsedrlllylpfdrpreelkseetleesefllk 180
QY 180 LHPYKSFLLDTLSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPSWATEDAMIKELSE 239
DB 181 lhpysflldtlsslsgfdqdlfglmskvydplfcesvhnftlpswatedamikelse 240
QY 240 LSLSYGIHKKKESRLOGGVLVNEILKNMKLATOPQKYLWYSANDTIVSGIOMAL 299
DB 241 lsllsygihkksrloggvlnelknmklatqpkykklwysandtvtsglqmal 300
QY 300 DVYNGVLPYASCHMMELCYHDKGFVEMYRNETQNEPYPLTLPGCTHSCPLEKFAELL 359
DB 301 dvyngvlpypaschmmelyhdkgfhvemyrnetqnepypltlpgcthsoplekfaell 360
QY 360 DPVIPQDWATECMATSSHQGT 380
DB 361 gpvipqdwatecmatsshggt 381

RESULT 3
AAW95081 standard; Protein: 386 AA.
ID AAW95081

```

XX AA095081;
AC 20-MAY-1999 (first entry)
XX Protein sequence Seq ID No: 47 from US 5882864.
DE
XX
XX Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;
KM differentiation; Reverse Transcription Polymerase Chain Reaction;
KM diagnostic; progression; cancer; metastasis; RT-PCR.
XX
XX Homo sapiens.
OS
XX US5882864-A.
XX
XX 16-MAR-1999.
XX
XX 31-JUL-1996; 96US-0692787.
XX
XX 31-JUL-1995; 95US-0001655.
XX 31-JUL-1996; 96US-0692787.
XX (UROC-) UROCOR INC.
XX
XX An G, O'Hara SM, Ralph D, Veltri R;
XX WPI: 1999-214055/18.
XX N-PSDB: AAX26062.
XX
XX Diagnosing prostate cancer and benign prostatic hyperplasia cells
XX using oligonucleotide probes specific for marker genes associated
XX with tumor differentiation and progression in Reverse Transcription
XX Polymerase Chain Reaction analysis
XX
XX Disclosure: Column 93-98; 74pp; English.
XX
XX The invention relates to methods for diagnosing prostate cancer or benign
XX prostatic hyperplasia cells in a biological sample. The method uses
XX oligonucleotides specific for marker genes associated with tumour
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful
XX for detecting and monitoring the progression of benign prostatic
XX hyperplasia and human prostate cancer (the most prevalent form of cancer
XX and a major cause of death in males) prior to the tumor undergoing
XX metastasis, therefore allowing the optimal method of treatment to be
XX determined before the condition becomes life threatening.
XX
XX Sequence 386 AA:
SQ

```

```

OY 300 DYNNGVLPYASCHMELVHDGCHFEVEMYRNETONEPYPLTLPCTHSCPLEKFAELL 359
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 dyngllppyschlelyfexgeyfvemyntehpylmlpgcspclietaelv 360
OY 360 DPVYIPDMATECMATSSHOCT 380
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 gvyipqdwstecmtntshgft 381

```

RESULT 4
AA59293
ID AA59293 standard; peptide; 386 AA.
AC AA59293;
XX
XX 19-APR-2000 (first entry)
XX
XX Prostatic acid phosphatase marker UC Band #47 amino acid sequence.
DE
XX Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;
KM benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection.
XX
XX Homo sapiens.
OS
XX WO964631-A1.
XX
XX 16-DEC-1999.
XX
XX 11-JUN-1999; 99WO-US13151.
XX
XX 12-JUN-1998; 98US-0097199.
XX
XX (UROC-) UROCOR INC.
XX
XX An G, O'Hara SM, Ralph D, Veltri RW;
XX WPI: 2000-116557/10.
XX N-PSDB: AAZ87547.
XX
XX Novel RNA biomarkers for diagnosis, prognosis and management of
XX prostate, breast and bladder cancer
XX
XX Example 2; Page 173-176; 191pp; English.
XX
XX The invention provides nucleic acid markers of prostate, breast and
XX bladder cancer. The markers are indicators of malignant transformation of
XX prostate, breast and bladder tissues and are diagnostic of the potential
XX for metastatic spread of malignant prostate tumours. The nucleic acid can
XX also be used as targets for therapeutic intervention in prostate cancer.
XX benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The
XX markers may be used to design specific probes and primers, for the rapid
XX analysis of prostate, bladder or breast biopsy samples. The probes and
XX primers may also be used for in situ hybridization or in situ PCR
XX detection and diagnosis. They may also be used to identify and isolate
XX full length gene sequences from various DNA libraries. Antibodies
XX against the polypeptide products of the markers can be used to treat
XX prostate cancer, bladder cancer or breast cancer. The encoded proteins
XX may be used to detect antibodies. The proteins and antibodies can be
XX used in immunodetection methods for detecting or quantifying the cancers,
XX and for clinical diagnosis of these cancers. The antibodies may also be
XX used for radioimaging to quantify and localize the encoded proteins.
XX
XX Sequence 386 AA:
SQ

Query Match 80.7%; Score 1661.5; DB 21; Length 386;
Best Local Similarity 81.6%; Pred. No. 1.9e-156;
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

```

OY 1 MGAIVPLPSPTASISGFIILLSLICDPPG-OAKELKFTLVPRHGRGPIETPTDPIITE 59
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 mraaplllaraaslsigfllflfwldrsvlaelkfvltvfhgdrspdtptdpik 60
OY 60 SSMPOFGOLTOGMBQDHYELSGYIRKRYGRFLNDTYKHDQYIRSTVDYRTLSAMTNL 119
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 sswpggfgltqgmeghvelgeytkrykflnesykhgeylyrstdvdrtlmsamtnl 120
OY 120 AALFPEEGISINNPRLWOPIPVHYVLSBDRLLYLPFRDCPFEEELKSTLESEFLKR 179
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 aalfpgegyslwnpdlwqplpvtvplsedqlllylfrncprfgelesetlkseeffqxr 180
OY 180 LHPYKSLFDTLSLSGFDODDLFGIMSKYVDPPLFCESVHNHFTLPPSNATEDAMIKLELSE 239
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 lhpkykfictlqklsghqgdltgswskvdydpcesvhnftlpsvatedumkklteise 240
OY 240 LSLSLGYIHOKKESKRSLOGVVLNIELKNMKLATOPORYYKKLVMYSAHDTYVSGLOMAL 299
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 lslslgyihkqkexerlsgyvlvnelnhmkratqlpsykkklmlysahtdtvsglqmal 300

```

Qy	60	SSMPQGFQGLITQMGKGEONHYLEGSTRKRYKGFLENDYTKKHDOITYRSDVDRTLMASANTNL	119
Db	61	sswpgifgdlitqlgmeghyelqeylfrkyrkflnesykhqevylrstvdvrtlmsantnl	120
Qy	120	AALFPEEGISINPRLWQPIVPHVSLSEEDRLYLPRPDCPREELKSEPLSESEFLKR	179
Db	121	aalfppegysinprlllwqprlvphvpsedqlllylprtmcprrqelsetlksseefqkr	180
Qy	180	LHPYKSFLLDTLSSLSGFDQDLFGIWSKVYDPLFCESVHNFTLPSMATEDAMIKELISE	239
Db	181	lhpykdfllatlgklsqllngqdlfgjwskvypriycesvhnftlpswatedmklrelse	240
Qy	240	LSLLSLYGHKHKESRSRLOGGVLVNEILKNNKLATPOKRYKKLYMSAHDTYSGLOMAL	299
Db	241	lsllsllyghkhkexsrllqggvllvneillnnmkrtqlpsykkllmysahdtlvsqldmal	300
Qy	300	DVYNGVLPYPYASCHMELLYHKGGFHEVEMYRNFTQNEPPYDLTLPGCTHSQPLEKFAEL	359
Db	301	dvyngdlppyaschltelyfkekgfhevemyrnetcqhpyplmpgcsplerfaely	360
Qy	360	DPVLPQDMATECMATSSHQT 380	
Db	361	gpvlpqdwatecmctmshqtr 381	
RESULT 5			
AAW19762			
ID	AAW19762	standard; Protein: 515 AA.	
AC	AAW19762;		
XX	17-SEP-1997	(first entry)	
DE	PAP-GM-CSF Immunostimulatory fusion protein.		
XX			
KW	PAP-GM-CSF; granulocyte macrophage colony stimulating factor;		
KM	prostatic acid phosphatase; tumour-specific antigen;		
XX	immunostimulant; prostate cancer; immunisation; therapy.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..32	
FT		/label= "Sig_peptide"	
FT		/note= "PAP signal peptide"	
FT	Protein	33..515	
FT		/label= "Mat_Protein"	
FT		/note= "PAP-GM-CSF fusion"	
FT	Protein	33..386	
FT		/label= "PAP"	
FT	Peptide	387..388	
FT		/label= "Linker"	
FT	Protein	/note= "product of BamHI linker"	
FT		389..515	
FT		/label= "GM-CSF"	
FT	Disulfide-bond	161..372	
FT		215..313	
FT	Disulfide-bond	347..351	
FT	Disulfide-bond	442..484	
FT	Disulfide-bond	476..509	
FT	Modified-site	94	
FT		/label= "Glycosylation"	
FT		/note= "potential N-glycosylation site"	
FT	Modified-site	220	
FT		/label= "Glycosylation"	
FT		/note= "potential N-glycosylation site"	
FT	Modified-site	333	
FT		/label= "Glycosylation"	
FT		/note= "potential N-glycosylation site"	
FT	Modified-site	415	
FT		/label= "Glycosylation"	
FT		/note= "potential N-glycosylation site"	

FT	Modified-site	425	/label= Glycosylation
FT			/note= "potential N-glycosylation site"
XX			
PN	WO9724438-A1.		
XX			
PD	10-JUL-1997.		
XX			
PF	23-DEC-1996;	96WO-US20241.	
XX			
PR	28-DEC-1995;	95US-0579823.	
XX			
PA	(ACT1-) ACTIVATED CELL THERAPY INC.		
XX			
PI	Laus R, Ruegg CL, Wu H;		
XX			
DR	WPI: 1997-363674/33.		
DR	N-PSDB: AAT72721.		
XX			
PT	Potent APC that activates T-cells to give multivalent cellular		
PT	immune response - can also induce a cytotoxic T-cell response in a		
PT	vertebrate subject		
XX			
PS	Example 1; Fig 2; 45pp; English.		
XX			
CC	A fusion protein (AAW19762) comprises human prostatic acid		
CC	phosphatase (PAP, a tumour-specific antigen) and granulocyte-		
CC	macrophage colony stimulating factor (GM-CSF). It is the		
CC	expression product of a nucleic acid molecule (AA772721) prep'd. by		
CC	PCR amplification of PAP GM-CSF cDNAs and their fusion via a BamHI		
CC	linker. Fusion expression vectors can be used to transfect		
CC	mammalian and insect cells. The PAP-GM-CSF fusion protein is used		
CC	to induce anti-PAP immunity. PAP serves both as an inducer of		
CC	cytotoxic T lymphocytes (CTL) and as a target for prostate cancer		
CC	cells when combined with the dendritic cell binding protein GM-CSF		
CC	and used to stimulate antigen presenting cells that are then used		
CC	to prime CTL.		
XX			
XX			
SQ	Sequence 515 AA;		
Query Match	80.7%; Score 1661.5; DB 18; Length 515;		
Best Local Similarity	81.6%; Pred.No. 3e-156;		
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;			
QY	1	MGAVPLPLSPRTSLSLGFLLLSLCLDPC-QAKELKFTVLVFRHGDGRPIETFPDPTTE	59
DB	1	mraaplllaraaasllgflilffvaldsvlakelkfvclvfrhgdgrpsidrfpcdpkpe	60
QY	60	SSWPQFGQLTQWNGEONHVELSGYIRKRYGRPLNDTYRHQDIYIRSTVDPTILMSAMTNL	119
DB	61	sswpqgfgqlqgmeghyelgeylrkryrklnmsyhegyllstvdtrlmsamcnl	120
QY	120	AALPPEGISITWNPRLMOPIDPVHTVSUSEDRLYLPRDCRFEELKSETLESEEPKLR	179
DB	121	aalffppegyslwnpdlmqplpvhcvlpisqdqlllpfnrcprfgeelkseeqfqr	180
QY	180	LHPYKSLFDLSSLGFPDDQLFGIWSKRYVDRPLFEESYHNFLPSPWATREDAMIRKELSE	239
DB	181	lhpykfdiaclqklsqllhgqdlfgiwskvypdpllyceesvhnflpawatedcltclrelse	240
QY	240	LSLSLSTYGHKKEKSRLOGGVLVNEILKNMKLATQPOKYYKLVWYSAHDTVSGLOAL	299
DB	241	lsllsltyghkkekssrlggvylvneillnmkrtacqlpsykkllmshndltcvsglqmal	300
QY	300	DVYNGVLPRPYASCHMMELYHDKGHFVENYXRNETQNEBPYPLTLPGCSPLLEFAELL	359
DB	301	dvyngllppyaaschltelyfekgeyfvemynneqhpaplmipgscpsopclerfaelv	360
QY	360	DVYIPQDMATECMATSSHOGT	380
DB	361	gvipdgwstecmtlnshgt	381

```
RESULT 6
ID AAB56451 standard; Protein: 216 AA.
AC AAB56451;
DT 13-MAR-2001 (first entry)
DE Human prostate cancer antigen protein sequence SEQ ID NO:1029.
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
OS Homo sapiens.
PN WO20005174-A1.
PD 21-SEP-2000.
PF 08-MAR-2000; 2000MO-US05988.
PR 12-MAR-1999; 99US-0124270.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
PI Rosen CA, Ruben SM;
PI WPI: 2000-587513/55.
DR N-PSDB; AAF15654.
XX
XX Prostate cancer associated gene sequences, referred to as prostate
XX cancer antigens, useful for treatment, prevention, and diagnosis of
XX disorders such as prostate cancer -
XX
XX Claim 11; Page 1458-1459; 2338pp; English.
XX
XX AAF1566 to AAF1605 encode the human prostate cancer associated
XX proteins, called prostate cancer antigens, given in AAB5663 to AAB57302.
XX The prostate cancer antigens can have neuroprotective, cytosolic,
XX cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
XX nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
XX and can be used in gene therapy. The prostate cancer antigen
XX polynucleotides may be used for detection of prostate cancer, chromosome
XX identification, as chromosome markers, and for numerous other diagnostic
XX or research purposes. The prostate cancer antigens may be used to treat
XX disorders such as neural, immune, muscular, reproductive,
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX disorders, wounds, and infectious diseases. AAF1606 to AAF1614 to
XX AAB57303 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 216 AA;
SQ
```

```
DB 121 ttvsglqmdalvnyngllppryaschltelyfekgeyfvemrymetqhepylmlpccps 180
QY 350 CPLEKFAELLDPVLPDQWATECMATSSHOGT 380
DB 181 cpleraelvgvlpqdwatecmtnshgt 211

RESULT 7
ID AAG00216 standard; Protein: 210 AA.
AC AAG00216;
DT 06-OCT-2000 (first entry)
DE Human secreted protein, SEQ ID NO: 4297.
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
OS Homo sapiens.
PN EP1033401-A2.
PD 06-SEP-2000.
PR 21-FEB-2000; 2000EP-0200610.
PA 26-FEB-1999; 99US-0122487.
PA (GEST) GENSET.
PI Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI: 2000-500381/45.
DR N-PSDB; AAC00222.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 4297; 71pp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
XX of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX were prepared from total human RNAs or polyA+ RNAs derived from 30
XX different tissues. EST sequences usually correspond mainly to the 3'
XX untranslated region (UTR) of the mRNA because they are often obtained
XX from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX those cases where longer cDNA sequences have been obtained, the full 5'
XX UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX ends and can therefore be used to obtain full length cDNAs and genomic
XX DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX chromosome mapping procedures. They are used to obtain upstream
XX regulatory sequences and to design expression and secretion vectors.
XX
XX Sequence 210 AA;
SQ
```

Query Match 42.7%; Score 880.5; DB 21; Length 210;
Best Local Similarity 80.0%; Pred. No. 2,8e-79;
Matches 168; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

```
QY 1 MGAVPLPSPASTSLGFLLLSLCLDPG-QAKELFVTLVFRHGRGPRFETPTPTPE 59
DB 1 mraaplllraaslsqflflflfwldrsylakelhfvlvtlvtngsrspdtlcpbpke 60
QY 60 SSWPQGFQGLTQWGMQVHLEGLSIRKRYGRFLNDYKHKDQIYRSTDVDTLMSANTNL 119
DB 61 sswpgfgqtlqtgmegqhyelgelyirkryrkflneasykheqvylrstddrtlmsamtl 120
```


[illegible]

	Query Match	15.3%	Score 315.5;	DB 21;	Length 421;
	Best Local Similarity	26.9%;	Pred. No. 1.le-22;		
	Matches 116;	Conservative 62;	Mismatches 155;	Indels 99;	Gaps 20;
OY	16 IGFLLLSICLD-----PGQAK-----ELKFTLVFNRGDBGPIETPTD--	55			
	: : :	:	: : :	:	:
Db	7 yvvltslayclhrrvalaelqeaagdcgpcvdrtllklkmvgvftrngarsplkpijleeq	66			
OY	56 -----PITSSW-----PGSF-----GQLRWNGMEQHIX	78			
	: : :	:	: :	:	:
Db	67 vempqllevpqbtfdyvtlnlaagbpkyrpsdydqynettlkgmfaaglkckvymgnmf	126			

```

0Y  79  ELG5TRKRRCY---FLMDTKRKHQOYIRSDVDVRLMSANTNLALF--PPRCISIMNP 133
   |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 127  algerlkrnyvedlpflsptfmpbevfrfnsitfrnlestrcollaglfqocqeg----- 180
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

0Y 134  RLMMQPIVHVYLSUEDLLTLPPEDDCPRFELKSETLESEEFKLRLHPRKSFJDLTSSL 193
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 181  ----piliht-deadseviypnysc--wslqrtrgrqrqtslqpgisedlkkvkd 231
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

0Y 194  SGFDQDDJFGIMSKVYDPLFCESYHNFTLPSMATEDAMIKKLELSLSLSTLCIGHKO-K 252
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 232  mgidsdskdvffli-llhvaaeqahn--lpscpmlkrfarmlegravd-etsylplpredr 287
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

0Y 253  EKSRLQGG---VLVNEILKNNKLATOPQRYKKLVMYSAHDITVSGLOMALDYNGVLP 308
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 288  eslgnmavpflhllesnllkamsatsapdktrkilylaahdvtfipllmtlglftkwpp 347
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

0Y 309  YASCHMELIYH--DKGGEFVEKRYRNEIQNRPYFLTL-GETHS-CPLEKFAELLD--PV 362
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 348  fawdltmlelyghleskewefvjylhygkeq-----vprgpcpdlcpdlmflnamsvytl 400
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

0Y 363  IPQDMATECMAT 374
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 401  spekynhalcsqt 412
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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RESULT	11
AA13368	
ID	AA13368 standard; Protein; 428 AA.
XX	
AC	AA13368;
XX	
DT	25-JUN-1999 (first entry)
XX	
DE	Amino acid sequence of protein PRO231.
XX	
KW	Secretd protein; transmembrane protein; human; enterocolitis;
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW	congenital microvillus atrophy; skin disease; cell growth;
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW	fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW	anti-chromoblastic; wound healing; tissue repair.
XX	
OS	Homo sapiens.
XX	
PN	W09914328-A2.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998; 98WO-US19330.
XX	
PR	25-NOV-1997; 97US-0066840.
PR	17-SEP-1997; 97US-0059113.
PR	17-SEP-1997; 97US-0059115.
PR	17-SEP-1997; 97US-0059117.
PR	17-SEP-1997; 97US-0059119.
PR	17-SEP-1997; 97US-0059121.
PR	17-SEP-1997; 97US-0059122.
PR	17-SEP-1997; 97US-0059184.
PR	18-SEP-1997; 97US-0059263.
PR	18-SEP-1997; 97US-0059266.
PR	15-OCT-1997; 97US-0062125.
PR	17-OCT-1997; 97US-0062285.
PR	17-OCT-1997; 97US-0062287.
PR	21-OCT-1997; 97US-0063486.
PR	24-OCT-1997; 97US-0062814.
PR	24-OCT-1997; 97US-0062816.
PR	24-OCT-1997; 97US-0063045.
PR	24-OCT-1997; 97US-0063120.
PR	24-OCT-1997; 97US-0063121.
PR	24-OCT-1997; 97US-0063127.
PR	27-OCT-1997; 97US-0063128.
PR	27-OCT-1997; 97US-0063329.

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PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063554.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 31-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 03-NOV-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0064809.
PR 17-NOV-1997; 97US-0065186.
PR 18-NOV-1997; 97US-0065846.
PR 21-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066372.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066710.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
PA (GETH ) GENENTECH INC.
XX
XX
XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX WPI: 1999-229533/19.
XX DR N-PSDB: AAX52239.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
XX
XX Claim 12; Fig 52; 320pp; English.
XX
XX AA113344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
CC ulceration and congenital microvillus atrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophia areata; PRO266 can be used as an
CC anti-thrombotic agent; PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC be used for treating problems of the kidney, uterus, endometrium, blood
CC vessels, or related tissue, e.g. in the heart of genital tract.
XX
XX
XX Sequence 428 AA:
50
Query Match 15.3%; Score 315.5; DB 20; Length 428;
Best Local Similarity 26.9%; Pred. No. 1.1e-22;
Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;
16 LGFLLLSLCLD-----PEQAK-----ELKVTLVFRRGRDGPETPTD-- 55
: : : : : : : : : : : : : : : : : : : : : : : : : : :
14 YGLTSLAYCQLHRYVAELQADGGQCPVDLSLKLKMGVYFTRGASPLKPLLEQ 73

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Oy	56	-----PIRESH-----PGF-----GOLTIOMGEQHY 78
Db	74	wemppqllvppbqcfidyvlnlagaipkpyrpsdqyhetcllkgmfagqclkvgmqmf 133
Oy	79	ELGSYIRKRYR---FLNDDTYKNDQIYIRSDVDRTLMSAMTNLALF--PREGISINMP 133
Db	134	algetrlnyvedrpfisrptpgevftrstlnfnlslgcllagaifgcqkeg----- 187
Oy	134	RLMWRPVDHTVLSSEDRLLYLPRDRCPREELKSETLSEEFRLKRLNRPYKSFDTLSSL 193
Db	188	-----plllht-deadseevlypnqsc---wsrlgrtgrgrtaslqpslssclkkvkdr 238
Oy	134	SGFDQDDLFGLMSKVYRPLRCESYHNNTLRSMKTEBDAMIKKLSSLSLSLXGINKQ-k 252
Db	239	mgldsdcdvdfdl-ldnvaeeqah--lpscmklxrfarmlegravd-tslyl1pkedr 294
Oy	253	EKSRLQGC---VIVNELIKNMKLTATOPQKKLVMSAHDTVSGLOMALDVNGVLPR 308
Db	255	eslqmwavprfllhlesnllkamdsatarpdklrlklyyaahdvtfrrllmclgfdfkwp 354
Oy	309	YASCHMELVH-DKSGHFEMVYURNETQNEPYRLTLR-GCTHS-CRLEFAEELD--PV 362
Db	355	favdtlmevlyhleskewfvqlyyhqeg-----vprsgpgrldpdmflnamsvyl 407
Oy	363	IPDMATECMAT 374
Db	408	spekhyalcsgt 419
RESULT 12		
AAB24399		
ID	AAB24399 standard; Protein; 428 AA.	
XX	AAB24399;	
AC	07-NOV-2000 (first entry)	
XX	Human PRO231 protein sequence SFQ ID NO:56.	
DE	Human	
XX	Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;	
KW	diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;	
KW	angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;	
KW	cytostatic; gene therapy; vaccine.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200032221-A2.	
PN	08-JUN-2000.	
XX	30-NOV-1999; 99WO-US28313.	
XX	01-DEC-1998; 98WO-US25108.	
XX	16-DEC-1998; 98US-0112850.	
PR	12-JAN-1999; 99US-0115554.	
PR	08-MAR-1999; 99WO-US05028.	
PR	12-MAR-1999; 99US-0123957.	
PR	28-APR-1999; 99US-0131445.	
PR	14-MAY-1999; 99US-0134287.	
PR	02-JUN-1999; 99WO-US12252.	
PR	23-JUN-1999; 99US-0141037.	
PR	20-JUL-1999; 99US-0144758.	
PR	26-JUL-1999; 99US-0145698.	
PR	01-SEP-1999; 99WO-US20111.	
PR	08-SEP-1999; 99WO-US20594.	
PR	13-SEP-1999; 99WO-US20944.	
PR	15-SEP-1999; 99WO-US21090.	
PR	15-SEP-1999; 99WO-US21547.	
PR	05-OCT-1999; 99WO-US23089.	
PR	29-OCT-1999; 99US-0162506.	
XX	(GETH) GENENTECH INC.	

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
 PI Watanabe CK, Williams PM, Wood WT;
 XX WPI: 2000-412154/35.
 DR N-PSDB: AAA77553.
 XX
 PT Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating a cardiovascular, endothelial or
 PT angiogenic disorders in mammals -
 XX
 PS Claim 72; Fig 24; 315pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating a
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PRO expression such as cardiovascular, endothelial or
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 428 AA;

Query Match 15.3%; Score 315.5; DB 21; Length 428;
 Best Local Similarity 26.9%; Pred. No. 1.1e-22;
 Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;

QY 16 LGFLLLSLCID-----PGQAK-----ELKFTLVGRHGRDRIETFPD-- 55
 DB 14 vgytstlayclhqrvalaelgeadgqcpvdrslklkmqvvrfrngarplprieq 73
 QY 56 -----PTESSW-----PGGF-----GOLTOGMEOHY 78
 DB 74 vewnpqllevpqtqdytvtlnlaggpkpyspdyqshettlkgmtaagqltkvngqm 133
 QY 79 ELGSYTRKRYGR--FLNDTYKHQIYIRSTVDYRLTMSAMTALAFL--PPEGISIMNP 133
 DB 134 algerlrknyvedlplspfrpgevfirtnfnlestrcllaglfgcqqeg----- 187
 QY 134 RLMOPIPHVTSLSDRLYLPRFOCPREELKSETLESEFLKRLHPRKSLDTLSSL 193
 DB 188 ----pilhlt-deadsevlvrypnygsc--wsrlrqrtrgrqaslpqysedlkkvkd 238
 QY 194 SGFDPDQLFCIGMSKVYDPLFCESVHNFTLPSWATEDAMIKLSELSLTVGIHKO-K 252
 DB 239 mgtdssdkvdfllldnvaagahn--lpscmklrfamiqgravd-tslylilkedr 294
 QY 253 EKSRLGG---VLVNEILKNMKLATQPKYKRLVMYSAHDTVSGIOMALDVYNGVLP 308
 DB 295 eslgmavgpflhlesnllkmdsatapdkrlklylaahdvffplmltliglfdhkwp 354
 QY 309 YASCHMELIYH--DKGHHYEMRYRNETQNEPRLPLP--GCTHS--CPLEFAELLD--PV 362
 DB 355 faudlmeqlqsheskwetvqlyhygkeg-----vrycpdgldcpldmflnamsvytl 407
 QY 363 IPQDMATECMAT 374
 DB 408 spekyhalcsqt 419

AC AAB80236;
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO231 protein.
 XX
 KW Human: PRO: dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiangiotensin nootropic; neuroprotective; vulnerrary; cardiant;
 KW antianxiogenic; vasotropic; antiaesthetic; antineumatic; cancer;
 KW antiarthritic; antidiabetic; antidiabetic; antidiabetic; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX
 OS Homo sapiens.
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000MO-US04414.
 XX
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 08-SEP-1999; 99MO-US20594.
 PR 13-SEP-1999; 99MO-US20944.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.
 PR 05-OCT-1999; 99MO-US23089.
 PR 29-NOV-1999; 99MO-US28214.
 PR 30-NOV-1999; 99MO-US28313.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 20-DEC-1999; 99MO-US30999.
 PR 05-JAN-2000; 99MO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin J;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WT;
 XX
 DR WPI: 2001-081051/09.
 DR N-PSDB: AAF72397.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 XX
 PS Claim 1; Fig 52; 393pp; English.
 XX
 CC The present sequence is one of sixty one novel secreted and
 CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding, angiogenesis, ischaemias such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 428 AA;

Query Match 15.2%; Score 313.5; DB 22; Length 428;
 Best Local Similarity 26.4%; Pred. No. 1.8e-22;
 Matches 114; Conservative 63; Mismatches 156; Indels 99; Gaps 19;

PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083352.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
DR N-PSDB; AA24217.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,

PT useful for treating blood coagulation disorders, cancers and cellular
PR adhesion disorders -
XX
PS Claim 12; Fig 155; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 480 AA;

Query Match 10.1%; Score 208.5; DB 20; Length 480;
Best Local Similarity 19.8%; Pred. No. 5, 7e-12;
Matches 84; Conservative 62; Mismatches 127; Indels 151; Gaps 15;

QY 33 ELKFVTLVFRHGRGP----- 48
DB 87 klvsnvfifrhgdrplyvlpktrpeidctlvankrkyhpkleaflsmkskgasfes 146
QY 49 ----IEFPDPTTESWPGFCOLQWQMEQHYELGSYTRKRY---GRPLNDPTYKHQI 101
DB 147 plnslpynphplce-----mgeltqgyvqhngqllrdlylkkhklpndwaadql 200
QY 102 YIRSTDVRTLSAMTNLAALPPREGISIWNPRLMQPIVHVVSUSEDRLLYLPFRD-- 159
DB 201 yletgtksrtlqsglallyflpd-----fdwkk-----yfrhqp 236
QY 160 -----CPRFEELKSTLESEELKRLHRYKSLDTLSLSGDDQDLGINSKY- 208
DB 237 saifcsgscycp---vngyleq-rrgy-----llfknsglekygemakiv 282
QY 209 -----YDPLFCESVHNFTLPSNATEDAMIKELSELSTLSTYGIHKOKK-- 254
DB 283 dypktqlraanpidsmchchvnsfp--ctnrgcvdmefkvikthqjedererrek 340
QY 255 ----SRLGGVLYNEILKNNKLATPQKRYKLVYSADHTVSGLOALDVYNGVLPYA 310
DB 341 yfgysllgahpnlngtigrmrategrkeelfalysahdvltlspalslglsaeafpfa 400
QY 311 SCHMMEIYHDK---GGEFVAMY-----RRETONREYPLTLPGCTHSCPLEKF 355
DB 401 arllfclwdgrekpsenhvrllyngvdtlftsfcdqdhkrspkpm-----cplnl 452
QY 356 AELL 359
DB 453 vrfv 456

Search completed: August 2, 2001, 18:18:46
Job time: 295 sec

Part of Article 34 Amendment
or is this a different Amendment

For a set of papers
with the Amendment

Don't know

Attorney

Over

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 2, 2001, 18:18:51 ; Search time 24.19 seconds

(without alignments)
2105.723 Million cell updates/sec

Title: US-09-402-845-2

Perfect score: 2060

Sequence: 1 MGAVPLPLSPFASLSLGLL.....DMATECMATSSHQGTGVALG 385

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_Organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_prodent:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2000	97.1	381	11	Q9QXH7	Q9qxh7 mus musculus
2	649	31.5	447	5	Q9U5U0	Q9u5u0 drosophila
3	649	31.5	447	5	Q9TVH9	Q9tvh9 drosophila
4	648	31.5	447	5	Q9U5U4	Q9u5u4 drosophila
5	648	31.5	447	5	Q9U5T9	Q9u5t9 drosophila
6	648	31.5	447	5	Q9U5T7	Q9u5t7 drosophila
7	647.5	31.4	447	5	Q9U5T8	Q9u5t8 drosophila
8	647	31.4	447	5	Q9U5U6	Q9u5u6 drosophila
9	646	31.4	447	5	Q9U5U1	Q9u5u1 drosophila
10	645	31.3	447	5	Q9U5T8	Q9u5t8 drosophila
11	645	31.3	447	5	Q9U5T5	Q9u5t5 drosophila
12	645	31.3	447	5	Q9U5T2	Q9u5t2 drosophila
13	645	31.3	447	5	Q9U5T1	Q9u5t1 drosophila
14	645	31.3	447	5	Q9TVH9	Q9tvh9 drosophila
15	645	31.3	447	5	Q9TVX2	Q9tvx2 drosophila
16	644	31.3	447	5	Q9U5V1	Q9u5v1 drosophila
17	644	31.3	447	5	Q9U5V0	Q9u5v0 drosophila
18	644	31.3	447	5	Q9U5U9	Q9u5u9 drosophila
19	644	31.3	447	5	Q9U5U2	Q9u5u2 drosophila

20	644	31.3	447	5	Q9TW53	Q9tw53 drosophila
21	644	31.3	447	5	Q9TW40	Q9tw40 drosophila
22	644	31.3	447	5	Q9TW19	Q9tw19 drosophila
23	643	31.2	447	5	Q9U5U7	Q9u5u7 drosophila
24	643	31.2	447	5	Q9U5U5	Q9u5u5 drosophila
25	643	31.2	447	5	Q9U5T6	Q9u5t6 drosophila
26	643	31.2	447	5	Q9U5T4	Q9u5t4 drosophila
27	643	31.2	447	5	Q9U5T3	Q9u5t3 drosophila
28	641	31.1	447	5	Q9U5U3	Q9u5u3 drosophila
29	640	31.1	447	5	Q9U5U8	Q9u5u8 drosophila
30	640	31.1	447	5	Q9U5U8	Q9u5u8 drosophila
31	639	31.0	447	5	Q9U5U8	Q9u5u8 drosophila
32	638	31.0	447	5	Q9U5U8	Q9u5u8 drosophila
33	638	31.0	447	5	Q9U5S8	Q9u5s8 drosophila
34	637	30.9	447	5	Q9U5S9	Q9u5s9 drosophila
35	632	30.7	447	5	Q9U5U8	Q9u5u8 drosophila
36	616	29.9	438	5	Q9VAD0	Q9vad0 drosophila
37	567	27.5	392	5	Q9VVZ9	Q9vvz9 drosophila
38	487	23.6	410	5	Q9VW00	Q9vw00 drosophila
39	487	23.6	440	5	Q17373	Q17373 caenorhabdi
40	480	23.3	366	5	Q22630	Q22630 caenorhabdi
41	479	23.3	376	5	P90949	P90949 caenorhabdi
42	476	23.1	412	5	Q9VW01	Q9vw01 drosophila
43	468	22.7	344	5	Q20662	Q20662 caenorhabdi
44	384.5	18.7	395	5	Q9VD68	Q9vd68 drosophila
45	375	18.2	449	5	Q19076	Q19076 caenorhabdi

ALIGNMENTS

RESULT 1

Q9QXH7 PRELIMINARY; PRT; 381 AA.

AC Q9QXH7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PROSTATIC ACID PHOSPHATASE.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Crew M.D., Chatta G.S., Borg C.D.;

RT "Sequence and expression of mouse prostatic acid phosphatase.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF210243; AAF23171.1;

DR HSSP; P20646; IRPA.

DR InterPro; IPR000560;

DR Pfam; PF00328; acid_phosphat; 1.

DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.

DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

SQ SEQUENCE 381 AA; 43689 MW; 60AD6919D77CB241 CRC64;

Query Match 97.1%; Score 2000; DB 11; Length 381;
Best Local Similarity 98.7%; Pred. No. 6.2e-159;
Matches: 374; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGAVPLPLSPFASLSLGLL...LCLDPPGQAKELKLVTLVFRHGRGPIETFFTPDPTES 60

Db 1 MRAVPLPLSPFASLSLGLL...LCLDPPGQAKELKLVTLVFRHGRGPIETFFTPDPTES 60

QY 61 SWPQGFQQLTQWMEQHYELGSIYRKRYGRFLNDYTKHDIYIRSTVDVDTLSAMTNLA 120

Db 61 SWPQGFQQLTQWMEQHYELGSIYRKRYGRFLNDYTKHDIYIRSTVDVDTLSAMTNLA 120

QY 121 ALPPEGISIWNPRLLMQPIPVHTVVSLSRDLVLPDPCPRFEELKSETLESEELKRL 180

Db 121 ALPPEGISIWNPRLLMQPIPVHTVVSLSRDLVLPDPCPRFEELKSETLESEELKRL 180

```
Qy 181 HPKSFSLDTLSSLGFDQDDLFQWSKVYDPLFCESVHNFTLPSPWATEDAMIKLKEISEL 240
Db 181 HPKSFSLDTLSSLGFDQDDLFQWSKVYDPLFCESVHNFTLPSPWATEDAMIKLKEISEL 240
Qy 241 SLLSLYGIHKQKESRSGGVLVNEILKNMKLATQPKYKLYMSAHDITVSGLOMALD 300
Db 241 SLLSLYGIHKQKESRSGGVLVNEILKNMKLATQPKYKLYMSAHDITVSGLOMALD 300
Qy 301 YVNGVLPYASCHMWELVHDKGGHFVEMYRNQNEPYPLTLPCTHSCPLEKFAELLD 360
Db 301 YVNGVLPYASCHMWELVHDKGGHFVEMYRNQNEPYPLTLPCTHSCPLEKFAELLD 360
Qy 361 PVIQDWATECMATSSHQG 379
Db 361 PVIQDWATECMATSSHQG 379

RESULT 2
ID Q9U5U0 PRELIMINARY; PRT; 447 AA.
AC Q9U5U0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J34ST/054; PubMed=10511564;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
RT inferred from nucleotide variation at the AcpH-1 gene region of
RT Drosophila subobscura.";
RL Genetics 153:871-889(1999).
DR EMBL; AJ389443; CAB59941.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat. 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolyase.
SQ SEQUENCE 447 AA; 50998 MW; FB7CDB4E1EBE5840 CRC64;

Query Match 31.5%; Score 649; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 4.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PGQAKELKFTLVFRHGRGPIETPTDPTITSS-WPQGFQLTQWGMEOHYELGSIYRK 86
Db 54 PG---ELKFAHVI FRHGRTPVDPYPTDPNNRKFPTWPGQLNLGKEQHYELGKWL RN 110
Qy 87 RYGRFLNDTYKHDIYIRSTDVRTLSAMTNLAALFPPEGISINPRLLMQPIPVHTVS 146
Db 111 RYKSLGSRYNEDIFVQSTDVDRTLMSAQSDLAGLVEPQGDIDWNPRIQMPVHTVP 170
Qy 147 LSEDRLLYLPDRCPREELKSETLE-SEEFKLRLHPYKSFDTLSSLSG-----FDQ 199
Db 171 EKDSILAAK-ASCPAY-DYELATLEASSEFQALYVRYRELLSYLTQNSGRLVKSFIDAQ 228
Qy 200 DLFGIWSKVYDPLFCESVHNFTLPSPWATEDAMIKLKEISELSLLSYGIHKQKESRLOG 259
Db 229 YL-----NNTLFTIEKLYNMTLPWA--EKVYKKELTYVSNFAFSTATUTRSMARUKT 279
Qy 260 GVLVNEILK--NMKLATQPKYKLYMSAHDITVSGLOMALDVYNGVLPYASCHMMEL 317
Db 280 GPLKDLIFERDCKLNQKLPDRSLWIYSAHDTTIANVLNSLKLFEHSPYAAACIMLEM 339
Qy 318 -YHDKGGHFVEMYRNQNEPYPLTLPCTHSCPLEKFAELLDVPIQDWATEC----M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLKTLVKLYQDVLPPVNNERECKRSTM 398
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Db 280 GPLKDLIFERDCKLNQKLPDRSLWIYSAHDTTIANVLNSLKLFEHSPYAAACIMLEM 339
Qy 318 -YHDKGGHFVEMYRNQNEPYPLTLPCTHSCPLEKFAELLDVPIQDWATEC----M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLKTLVKLYQDVLPPVNNERECKRSTM 398
Qy 373 ATSSHQGTGVA 383
Db 399 MMTYEANLGA 409

RESULT 3
Q9TVH9
ID Q9TVH9 PRELIMINARY; PRT; 447 AA.
AC Q9TVH9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALST/054; AND J8ST/054;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
RT inferred from nucleotide variation at the AcpH-1 gene region of
RT Drosophila subobscura.";
RL Genetics 153:871-889(1999).
DR EMBL; AJ389447; CAB59945.1; -.
DR EMBL; AJ389446; CAB59944.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat. 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolyase.
SQ SEQUENCE 447 AA; 51040 MW; E1CCDB4E0FAF5851 CRC64;

Query Match 31.5%; Score 649; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 4.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PGQAKELKFTLVFRHGRGPIETPTDPTITSS-WPQGFQLTQWGMEOHYELGSIYRK 86
Db 54 PG---ELKFAHVI FRHGRTPVDPYPTDPNNRKFPTWPGQLNLGKEQHYELGKWL RN 110
Qy 87 RYGRFLNDTYKHDIYIRSTDVRTLSAMTNLAALFPPEGISINPRLLMQPIPVHTVS 146
Db 111 RYKSLGSRYNEDIFVQSTDVDRTLMSAQSDLAGLVEPQGDIDWNPRIQMPVHTVP 170
Qy 147 LSEDRLLYLPDRCPREELKSETLE-SEEFKLRLHPYKSFDTLSSLSG-----FDQ 199
Db 171 EKDSILAAK-ASCPAY-DYELATLEASSEFQALYVRYRELLSYLTQNSGRLVKSFIDAQ 228
Qy 200 DLFGIWSKVYDPLFCESVHNFTLPSPWATEDAMIKLKEISELSLLSYGIHKQKESRLOG 259
Db 229 YL-----NNTLFTIEKLYNMTLPWA--EKVYKKELTYVSNFAFSTATUTRSMARUKT 279
Qy 260 GVLVNEILK--NMKLATQPKYKLYMSAHDITVSGLOMALDVYNGVLPYASCHMMEL 317
Db 280 GPLKDLIFERDCKLNQKLPDRSLWIYSAHDTTIANVLNSLKLFEHSPYAAACIMLEM 339
Qy 318 -YHDKGGHFVEMYRNQNEPYPLTLPCTHSCPLEKFAELLDVPIQDWATEC----M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLKTLVKLYQDVLPPVNNERECKRSTM 398
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Qy 373 ATSSHQGTGVA 383
Db 399 MMTYEANLGA 409

RESULT 4

Q9U504 ID Q9U504 PRELIMINARY; PRT; 447 AA.
AC Q9U504
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J57ST/100;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
inferred from nucleotide variation at the AcpH-1 gene region of
Drosophila subobscura.";
RL Genetics 153:871-889(1999).
DR EMBL: AJ389437; CAB59935.1; -.
DR HSP: P15309; ZHPA.
DR FlyBase: FBgn0013885; Dsub\AcpH-1.
DR InterPro: IPR000560; -.
DR Pfam: PF00328; acid_phosphat; 2.
DR ProDom: PD003823; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51049 MW; D3E545BFB1301859 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;
Best Local Similarity 39.1%; Pred. No. 5.8e-46;
Matches 145; Conservative 67; Mismatches 129; Indels 30; Gaps 12;

Qy 28 PQAKELKFTVLRHGRGPIETFPDPTTSS-WPQFGQLTQWMEQHVELGSIYRK 86
Db 54 PG---ELKFAHVIHFRHGRDTPVDPTDPWNNRKFMTGWLTLNKGQHYELGKWL 110
Qy 87 RYGRFLNDYTKHDIYIRSTDVRTLSAMTNLAALPPGEGISLWNPRLWQIPVHTVS 146
Db 111 RYKSLGSRVTNEDIFVQSTDVRTLSAQSDLAGLYEPOGDDIWNPRIDWQPVVHTVP 170
Qy 147 LSEDRLLYLPFRDPCPRFEELKSETLESEEFKRLH-PYKSFLLTSLSG-----PDDQ 199
Db 171 EKDDSIILAAK-ASCPAY-DYELATLEASSEFHLVRYRELLSYLTQNSGRLVKSFIDAQ 228
Qy 200 DLFGWSKVYDPLFCESVHNFTLPSWATEDAMIKLSELSLSLYGIHKEKESRLQG 259
Db 229 YL-----NNTLFIEKLYNMTLPVWA--EKVYGKEELTYVSNFAFSTATFTSRMARLKT 279
Qy 260 GVLVNEILK--NMKLTQPKQYKLVMSAHDITVSGQALMDVYNGVLPPYASCHMMEL 317
Db 280 GPLLKDFEFDKLNQLKPDRLSLWISAHDTTIANVLSKLFLHSPYAAACIMLEM 339
Qy 318 -YHDKGGHFVEMYRYNETQNEPYPLTLPGCTHSCPLKFAELLDPIVPODWATEC-----M 372
Db 340 RVDDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLTKLVKLYQDLVLPVNWRECKRSTM 398
Qy 373 ATSSHQGTGVA 383
Db 399 MMTYEANLGA 409

RESULT 6

Q9U5T7 ID Q9U5T7 PRELIMINARY; PRT; 447 AA.
AC Q9U5T7

Query Match 31.5%; Score 648; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 5.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PQAKELKFTVLRHGRGPIETFPDPTTSS-WPQFGQLTQWMEQHVELGSIYRK 86
Db 54 PG---ELKFAHVIHFRHGRDTPVDPTDPWNNRKFMTGWLTLNKGQHYELGKWL 110
Qy 87 RYGRFLNDYTKHDIYIRSTDVRTLSAMTNLAALPPGEGISLWNPRLWQIPVHTVS 146
Db 111 RYKSLGSRVTNEDIFVQSTDVRTLSAQSDLAGLYEPOGDDIWNPRIDWQPVVHTVP 170
Qy 147 LSEDRLLYLPFRDPCPRFEELKSETLE-SEEFKRLHYPKSFLLTSLSG-----PDDQ 199
Db 171 EKDDSIILAAK-ASCPAY-DYELATLEASSEFHLVRYRELLSYLTQNSGRLVKSFIDAQ 228
Qy 200 DLFGWSKVYDPLFCESVHNFTLPSWATEDAMIKLSELSLSLYGIHKEKESRLQG 259
Db 229 YL-----NNTLFIEKLYNMTLPVWA--EKVYGKELTYVSNFAFSTATFTSRMARLKT 279
Qy 260 GVLVNEILK--NMKLTQPKQYKLVMSAHDITVSGQALMDVYNGVLPPYASCHMMEL 317
Db 280 GPLLKDFEFDKLNQLKPDRLSLWISAHDTTIANVLSKLFLHSPYAAACIMLEM 339
Qy 318 -YHDKGGHFVEMYRYNETQNEPYPLTLPGCTHSCPLKFAELLDPIVPODWATEC-----M 372
Db 340 RVDDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLTKLVKLYQDLVLPVNWRECKRSTM 398
Qy 373 ATSSHQGTGVA 383
Db 399 MMTYEANLGA 409

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A4ST/054;
RA MEDLINE=99442390; PubMed=10511564;
RX Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozymes and chromosomal polymorphism
inferred from nucleotide variation at the AcpH-1 gene region of
Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL; AJ389448; CAB59946.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51088 MW; A80B027ACA8D9279 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 5.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PQQAKELKFTLVFRHGDRGPIETPTDITESS-WPQGFQLTQMGMEQHYELGSGYIRK 86
|| |||| :||||| : : |||| || |||| : |||| : |||| : ||||
Db 54 PG---ELAFHVIHRGDRTPVDYPTDPWNNRKFWPTGWGQLTNLGKEQHYELGKWLNR 110
Qy 87 RYGRFLNDYKHDOYIIRSTVDRTLSAMTNLAALFPEGISINWRLLWQPIPVHTVS 146
|| || : : : : : ||||| |||| : |||| : |||| : |||| : ||||
Db 111 RYKLSGRYTNEDIFVOSTVDRTLSAQSLAGLYEPQGDIDWNRIDWQVPVHTVP 170
Qy 147 LSEDRLLYLPFRDCPRFELKSETLE-SEEFKRLRHPYKSFDTLSSLSG-----FDQ 199
: || : || : || : || : || : || : || : || : || : || : ||
Db 171 EKDDSIILAAK-ASCPAY-DYELATLEASSEFOALVRYRELLSYLTQNSGRVLSFIDAQ 228
Qy 200 DLFGTWSKYVDPLFCESVHNFTLPSNATEDAMIKUKELSELSSLXLYGIHKQKSRLOQ 259
: || : || : || : || : || : || : || : || : || : || : ||
Db 229 YL-----NNTLFTEKLYNMTLPVWA--EKVYGGKELTYVSNFAFSIATETRSMARLKT 279
Qy 260 GVLVNEILK--NMKLATOPQYKLVMSYSAHDTTVSGLOMALDVYNGVLPYASCHMMEL 317
|| : : : : : || : || : || : || : || : || : || : || : || : ||
Db 280 GPLLKDIFERFDKLNQNLKPDRLSIYSAHDTTIANVLSLKLFLHSPPYAACIMLEM 339
Qy 318 -YHDKGGHFVEMYRYNETQNEPYPLPGCTHSCPLEKFAELLDPIVPODWATEC---- 372
|| : || : || : || : || : || : || : || : || : || : ||
Db 340 RYDSDNTPLVSFVYKNTTA-EPLPLDIPGCGLSCLPLTLVKLYQDVLVFNWRECKRSTM 398
Qy 373 ATSSHQGVTVGA 383
Db 399 MMTYEANLGA 409

RESULT 7
OS Drosophila guanche (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
AC O97168; PRELIMINARY; PRT; 447 AA.
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J51ST/100;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7266;
RN [1]
RP SEQUENCE FROM N.A.
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The acid phosphatase-1 gene region in the Drosophila species of the
subobscura cluster."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18841; CAB38563.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0019218; Dgua\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51073 MW; 1950B73D3C0C8005 CRC64;

Query Match 31.4%; Score 647.5; DB 5; Length 447;
Best Local Similarity 37.4%; Pred. No. 6.4e-46;
Matches 154; Conservative 66; Mismatches 137; Indels 55; Gaps 13;

Qy 12 ASLSLGLFLLLS-----LCLDPGOAKELKFVTLVFRHGDR 46
|| : || : |||| : |||| : |||| : ||||
Db 13 ALLVIGVLCLLSFGIGNAVHIPTYGSGSEGETRPPDQATLPG---ELKFAHVIHRGDR 69
Qy 47 GPIETFTPTDITESS-WPQGFQLTQMGMEQHYELGSGYIRKRYGRFLNDYKHDOYIRS 105
|| : |||| : |||| : |||| : |||| : |||| : ||||
Db 70 TPVDYPTDPWNNRKFWPTGWGQLTNLGKEQHYELGKWLNRKYSLLGSRVTNEDIFVQS 129
Qy 106 TDVORTLSAMTNLAALFPEGISINWRLLWQPIPVHTVSLEDRLLYLPFRDCPREE 165
||||| |||| : || : || : || : || : || : || : || : || : || : ||
Db 130 TDVORTLSAQSLAGLYEPQGDIDWNRIDWQVPVHTVPEKDDSIILAAK-ASCPAY-D 187
Qy 166 LKSETLE-SEEFKRLRHPYKSFDTLSSLSG-----FDDQDLFGIWSKVVDPLFCESVH 218
|| : || : || : || : || : || : || : || : || : || : ||
Db 188 YELATLEASSEFOALVRYRELLSYLTQNSGRVLSFIDAQYL-----NNTLFIEKLY 240
Qy 219 NFTLPWSNATEDAMIKUKELSELSSLXLYGIHKQKSRLOGGVLYNEILK--NMKLATQP 276
|| || : : : || : || : || : || : || : || : || : ||
Db 241 NMTLPVWA--EKVGEKEELTYVSNFAFSIATETRSMARLKTGPLLKDIFERFDKLNQNL 298
Qy 277 QYKVKLVMSYSAHDTTVSGLOMALDVYNGVLPYASCHMMEL-YHDKGGHFVEMYRYNETQ 335
: : : ||||| : : : |||| : || : || : || : || : || : ||
Db 299 KPDRSLWTYSAHDTTIANVLSLKLFLHSPPYAACIMLEMRYDSDNTPLVSFVYKNTTA 358
Qy 336 NEPYPLTLPGCTHSCPLEKFAELLDPIVPODWATEC----NATSSHQGVTVGA 383
|| || : |||| : || : || : || : || : || : || : || : ||
Db 359 -EPLPLDIPGCGLSCLPLTLVKLYQDVLVFNWRECKRSTMMTYEANLGA 409

RESULT 8
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J51ST/100;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
```


"The relationship between allozyme and chromosomal polymorphism inferred from nucleotide variation at the Acph-1 gene region of *Drosophila subobscura*," Genetics 153:871-889(1999).

DR ENBL; AJ389432; CAB59930.1; -.
DR HSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\Acph-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
DR Hydrolase. 447 AA; 51049 MW; 10FABA5FAF6EEFF6 CRC64;
SQ SEQUENCE

Best local similarity 39.4%, Fied. NO. 1E-43;
Matches 146; Conservative 66; Mismatches 129; Indels 30; Gaps

QY 87 RYGRFLNDTYKXHDQIYIRSTVDVRTLMSAMTNLAALFFPEGISIWNPRLWQPIPVHTVS 146

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Db 111 RYKSLGSRVTNEDIFVQSTDVDRTLMSAQSLAGLYEPQGDIIWNPRIWQPVVHTVP 170
QY 147 LSEDRLLYLPFRDPCPEELKSETLE-SEEFKLRLHPYKSFELDTLSLSG-----FDDQ 199
Db 171 EKDDSLAAR-ASCPAY-DYELATLEASSEFQALYVRYRELLSYLTQNSRLVKSFIDAQ 228
QY 200 DLFGINSKVYDPLFCESVHNFTLPSPWATEDAMIKKLSLSLSSLYGIHKQEKSRLOQ 259
Db 229 YL-----NNTLFIKLYNNTLPVMA--EKVYKKEELTVVSNFATFTRSMARLKT 279
QY 260 GVLVNEILK--NNKLATOPQYKKLVMYSAHDTTVSGLOMALDVYNGVLPYPYASCHMEL 317
Db 280 GPLLKDIFERFDKLNQLKPDRLMIYSAHDTTIANVLNSLKLFEVHSPPYAACIMLEM 339
QY 318 -YHDKGCHVFEMRYRNETONEPYPLTLPCTHSCPLKFAELLDVPIPODWATEC---M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLTLVKLYQDVLPGNWERECKRSTM 398
QY 373 ATSHQCTGVA 383
Db 399 MMTYEEANLGA 409
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RESULT 13

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Q9U5T1
ID Q9U5T1 PRELIMINARY; PRT; 447 AA.
AC Q9U5T1;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
PT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J83(3+4)/100;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
inferred from nucleotide variation at the AcpH-1 gene region of
Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL; AJ389466; CAB59964.1; -.
DR HSSP; PI5309; ZHPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51049 MW; 3C5F45BFA3FDC325 CRC64;
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Query Match 31.3%; Score 645; DB 5; Length 447;
Best Local Similarity 39.1%; Pred. No. le-45;
Matches 145; Conservative 67; Mismatches 129; Indels 30; Gaps 12;

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QY 28 PGQAKELKFTVTLFRHGDGRPIETFTDPITESS-WPQFGQLTQMGMEQHYELGSYRK 86
Db 54 PG---ELKFAHVIFRIGDRTVPDPTDPNNRKFWPTGWLQNLGKEQHYELGKWLNR 110
QY 87 RYGRFLNDTYKHQDIYIRSTVDVDRTLMSANTLAALFPPEGISIWNPRLLWQPIPVHTVS 146
Db 111 RYKSLGSRVTNEDIFVQSTDVDRTLMSAQSLAGLYEPQGDIIWNPRIWQPVVHTVP 170
QY 147 LSEDRLLYLPFRDPCPEELKSETLESEEFKLRLH-PYKSFELDTLSLSG-----FDDQ 199
Db 171 EKDDSLAAR-ASCPAY-DYELATLESSEFQALYVRYRELLSYLTQNSRLVKSFIDAQ 228
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QY 200 DLFGINSKVYDPLFCESVHNFTLPSPWATEDAMIKKLSLSLSSLYGIHKQEKSRLOQ 259
Db 229 YL-----NNTLFIKLYNNTLPVMA--EKVYKKEELTVVSNFATFTRSMARLKT 279
QY 260 GVLVNEILK--NNKLATOPQYKKLVMYSAHDTTVSGLOMALDVYNGVLPYPYASCHMEL 317
Db 280 GPLLKDIFERFDKLNQLKPDRLMIYSAHDTTIANVLNSLKLFEVHSPPYAACIMLEM 339
QY 318 -YHDKGCHVFEMRYRNETONEPYPLTLPCTHSCPLKFAELLDVPIPODWATEC---M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLTLVKLYQDVLPGNWERECKRSTM 398
QY 373 ATSHQCTGVA 383
Db 399 MMTYEEANLGA 409
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RESULT 14

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Q9TW17
ID Q9TW17 PRELIMINARY; PRT; 447 AA.
AC Q9TW17;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
inferred from nucleotide variation at the AcpH-1 gene region of
Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL; AJ389461; CAB59959.1; -.
DR EMBL; AJ389450; CAB59948.1; -.
DR EMBL; AJ389453; CAB59951.1; -.
DR EMBL; AJ389454; CAB59952.1; -.
DR EMBL; AJ389460; CAB59958.1; -.
DR HSSP; PI5309; ZHPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51006 MW; 3D3A6472A73B12E1 CRC64;
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Query Match 31.3%; Score 645; DB 5; Length 447;
Best Local Similarity 39.4%; Pred. No. le-45;
Matches 146; Conservative 66; Mismatches 129; Indels 30; Gaps 12;

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QY 28 PGQAKELKFTVTLFRHGDGRPIETFTDPITESS-WPQFGQLTQMGMEQHYELGSYRK 86
Db 54 PG---ELKFAHVIFRIGDRTVPDPTDPNNRKFWPTGWLQNLGKEQHYELGKWLNR 110
QY 87 RYGRFLNDTYKHQDIYIRSTVDVDRTLMSANTLAALFPPEGISIWNPRLLWQPIPVHTVS 146
Db 111 RYKSLGSRVTNEDIFVQSTDVDRTLMSAQSLAGLYEPQGDIIWNPRIWQPVVHTVP 170
QY 147 LSEDRLLYLPFRDPCPEELKSETLE-SEEFKLRLHPYKSFELDTLSLSG-----FDDQ 199
Db 171 EKDDSLAAR-ASCPAY-DYELATLESSEFQALYVRYRELLSYLTQNSRLVKSFIDAQ 228
QY 200 DLFGINSKVYDPLFCESVHNFTLPSPWATEDAMIKKLSLSLSSLYGIHKQEKSRLOQ 259
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D6	229	YL-----NTLFIETKLYNMTLPVWA--EKVYGKEELTVYSNFASFIAITFTRSMARLKT	279
		: : : : : : : : : : : :	
QY	260	GVLVNEILK--NNKLATPQOKYKKLVMSAHDPTVSGLQWALDVNGVLPPVASCHMMEL	317
		: : : : : : : : : : : : : : : : :	
D6	280	GPLLKDIFERFDKKNLSQLKPDRSLMIYSADHTTIANVLSLKLFELHSPPYAACIMLEM	339
		: : : : : : : : : : : : : : : : :	
QY	318	-YHDGGHFVEMYRNFTONEPYPLPGCTHSCLPEAKFAELLDPVIPODWATEC----	372
		: : : : : : : : : : : : : : : : :	
D6	340	RVDSDNPPLVSVEFYKNTTA-EPFLPLDTPGGCLSPCLKTLVKLYQDVLPGNWERECKRSTM	398
		: : : : : : : : : : : : : : : : :	
QY	373	ATSSHOGTVCA	383
		: : : :	
D6	399	MMTYEEANLGA	409
		:	
RESULT	15		
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ID	Q9TVX2	PRELIMINARY;	PRT; 447 AA.
AC	Q9TVX2;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	ACID PHOSPHATASE-1 (EC 3.1.3.2).		
GN	ACPh-1.		
OC	Eukaryota suboscra (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephygiordeia; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7241;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=VARIOUS STRAINS;		
RC	MEDLINE=99442390; PubMed=10511564;		
RA	Navarro-Sabate A., Aguade M., Segarra C.;		
RT	"The relationship between allele variation at the Acph-1 gene region of		
RT	Inferred from nucleotide variation at the Acph-1 gene region of		
RL	Drosophila suboscra."		
RL	Genetics 153:871-889(1999).		
DR	EMBL; AJ389476; CAB60674.1; -		
DR	EMBL; AJ389472; CAB59970.1; -		
DR	EMBL; AJ389473; CAB59971.1; -		
DR	EMBL; AJ389474; CAB59972.1; -		
DR	HSSP; P15309; 2HPA.		
DR	FlyBase; FBgn013885; Dsub\Acph-1.		
DR	InterPro; IPR000560; -		
DR	Pfam; PF00328; acid phosphat; 2		
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.		
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.		
KQ	Hydrolase.		
SQ	SEQUENCE 447 AA; 50964 MW; 62E545C8BB5604FE CRC64;		

Qy	260	GVLYNEILK--NKLKATOPQKYKKLWMSYSAHDTTVSGLOWADVNGVLPYPYASCHMMEL	317
Db	280	GPLKLDIFERFDKLNQLKPDRLSWIYSAHDTTIANVLSNLSKLFELHSPPYAACIMLEM	339
Qy	318	-YHDKGGHFVEMYRYNETONEPYPLTLPGCTHSCPLEKFAELLDLPVLPQDWATEC----	372
Db	340	RVDDSNTPLSVFEYKNTTA-EPLPLDIPGGGLSCPLKTLVKLYQDVLPLGNWRECKRSTM	398
Qy	373	ATSSHQGTGVA	383
Db	399	MTTYEEANLGA	409

Search completed: August 2, 2001, 18:21:51
Job time: 180 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 2, 2001, 18:19:06 ; Search time 13.14 Seconds

(Without alignments)
1003.681 Million cell updates/sec

Title: US-09-402-645-2

Sequence: 1 MCAVPLPLSPATSLSLGFL.....DMATECMATSSHQTVGALG 385

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	88.2	381	1	P20646 ratius norv
2	1848	88.2	381	1	P20646 ratius norv
3	1848	88.2	381	1	P20646 ratius norv
4	1848	88.2	381	1	P20646 ratius norv
5	1848	88.2	381	1	P20646 ratius norv
6	1848	88.2	381	1	P20646 ratius norv
7	1848	88.2	381	1	P20646 ratius norv
8	1848	88.2	381	1	P20646 ratius norv
9	1848	88.2	381	1	P20646 ratius norv
10	1848	88.2	381	1	P20646 ratius norv
11	1848	88.2	381	1	P20646 ratius norv
12	1848	88.2	381	1	P20646 ratius norv
13	1848	88.2	381	1	P20646 ratius norv
14	1848	88.2	381	1	P20646 ratius norv
15	1848	88.2	381	1	P20646 ratius norv
16	1848	88.2	381	1	P20646 ratius norv
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18	1848	88.2	381	1	P20646 ratius norv
19	1848	88.2	381	1	P20646 ratius norv
20	1848	88.2	381	1	P20646 ratius norv
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22	1848	88.2	381	1	P20646 ratius norv
23	1848	88.2	381	1	P20646 ratius norv
24	1848	88.2	381	1	P20646 ratius norv
25	1848	88.2	381	1	P20646 ratius norv
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27	1848	88.2	381	1	P20646 ratius norv
28	1848	88.2	381	1	P20646 ratius norv
29	1848	88.2	381	1	P20646 ratius norv
30	1848	88.2	381	1	P20646 ratius norv
31	1848	88.2	381	1	P20646 ratius norv
32	1848	88.2	381	1	P20646 ratius norv
33	1848	88.2	381	1	P20646 ratius norv

ALIGNMENTS

RESULT	1	STANDARD	PRT	381 AA
PPAP_RAT				
AC	P20646;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).			
GN	ACPP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90323620; Pubmed=2373368;			
RA	Rolko K., Jaenke O.A., Vilko P.;			
RT	"Primary structure of rat secretory acid phosphatase and comparison to other acid phosphatases.";			
RL	Gene 89:223-229(1990).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).			
RX	MEDLINE=93327749; Pubmed=834986;			
RA	Schneider G., Lindqvist Y., Vilko P.;			
RT	"Three-dimensional structure of rat acid phosphatase.";			
RL	EMBO J. 12:2609-2615(1993).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).			
RX	MEDLINE=94012606; Pubmed=8407898;			
RA	Lindqvist Y., Schneider G., Vilko P.;			
RT	"Three-dimensional structure of rat acid phosphatase in complex with I(+)-tartrate.";			
RL	J. Biol. Chem. 268:20744-20746(1993).			
CC	-1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN			
CC	ALCOHOL + ORTHOPHOSPHATE.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: M32397; AAA41806.1; -			
DR	PIR: JH0152; JH0152.			
DR	PDB: 1RPA; 31-MAY-94.			
DR	PDB: 1RPT; 31-MAY-94.			
DR	InterPro: IPR000560; -			
DR	Pfam: PF00328; acid_phosphat; 1.			
DR	PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; FALSE_NEG.			
DR	PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.			
KM	Hydrolase; Glycoprotein; Signal; 3D-structure.			
FT	SIGNAL 1 31			

34	93.5	4.5	1103	1	CHS6_USRMA	O13395	usllago ma
35	93.5	4.5	1183	1	DRPL_RAT	P54258	rattus norv
36	93	4.5	465	1	TPSN_MOUSE	O97233	mus musculu
37	93	4.5	805	1	SUSY_MOUSE	O65026	medicago sa
38	92	4.5	655	1	AMYA_PYRAB	O9V298	pyrococcus
39	91.5	4.4	452	1	HOS2_YEAST	P53096	saccharomyc
40	91.5	4.4	467	1	PHYA_ASAPW	P34753	aspergillus
41	91.5	4.4	1185	1	DRPL_HUMAN	P54259	homo sapien
42	91.5	4.4	2717	1	ZEPI_HUMAN	P15822	homo sapien
43	91	4.4	536	1	DIT1_YEAST	P21623	saccharomyc
44	91	4.4	629	1	HAP1_RAT	P54256	rattus norv
45	91	4.4	805	1	SUSY_LYCES	P49037	lycopersico

FT CHAIN 32 381 PROSTATIC ACID PHOSPHATASE.
 FT DISULFID 160 371
 FT DISULFID 346 350
 FT ACT SITE 43 43
 FT ACT SITE 85 85
 FT CARBOHYD 93 93
 FT CARBOHYD 219 219
 FT CARBOHYD 332 332
 FT CARBOHYD 381 AA; 43850 MM; 5EEBFF67B062FE76 CRC64;
 SQ SEQUENCE

Query Match 88.3%; Score 1818; DB 1; Length 381;
 Best Local Similarity 88.5%; Pred. No. 7.6e-137;
 Matches 337; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 1 MCAVPLPSPSTSLSGFLLSLCLDPOAKELKFTLVFRRHGRGPEPEPTPTPTES 60
 DB 1 MAAYPLHLVGTASTLTLGLFLLSLRLDPOAKELKFTLVFRRHGRGPEPEPTPTPTES 60
 QY 61 SMPGEGQLTQMGMDQHYELGSIYIRKRYGRPLNDYTKHDQYIRSTVDVDTLSAMTALA 120
 DB 61 SMPGEGQLTKMGMDQHYELGSIYIRRYGRPLNNSYKHDQYIRSTVDVDTLSAMTALA 120
 QY 121 ALFPPREGISINMPRLIMQPIPVHTVSLSDRLILPFRCCPFREELKSTLESEFLKRL 180
 DB 121 ALFPPREGISINMPRLIMQPIPVHTVSLSDRLILPFRCCPFREELKSTLESEFLKRL 180
 QY 181 HPKKFLDTLSLSEGDODLFGISKSYVDPLFCESVNHFTLPSNATEDAMIKLELSEL 240
 DB 181 QPKKFLDTLSLSEGDODLFEIWSRLYDPLFCESVNHFTLRNATEDAMIKLELSEL 240
 QY 241 SLLSLGIHKOKESKRLQGLVNLNKLKMLATOPQYKYLKLVMSAHDTVSGIOMALD 300
 DB 241 SLLSLGIHKOKESKRLQGLVNLNKLKMLATOPQYKYLKLVMSAHDTVSGIOMALD 300
 QY 301 VYNGVLPYASCHMELTHDKGFVEYRNETONEPPLTLPGCTHSCPLEKFAELLD 360
 DB 301 LVNGLLPYASCHMELTHDKGFVEYRNETONEPPLTLPGCTHSCPLEKFAELLD 360
 QY 361 PYIPDMATECMATSSHOQTV 381
 DB 361 PYIPDMATECMATSSHOQTV 381

RESULT 2
 PPAP_HUMAN STANDARD: PRT: 386 AA.
 AC P15309;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
 GN ACP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92272747; PubMed=1375464;
 RA Sharief F.S., Li S.S.-L.;
 RT "Structure of human prostatic acid phosphatase gene";
 RL Biochem. Biophys. Res. Commun. 184:1468-1476(1992).
 RN [2]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, DISULFIDE BONDS, & ACTIVE SITE.
 RX MEDLINE=91115848; PubMed=1989985;
 RA van Etten R.L., Davidson R., Stevis P.E., MacArthur H., Moore D.L.;
 RT "Covalent structure, disulfide bonding, and identification of
 RT reactive surface and active site residues of human prostatic acid
 RT phosphatase";
 RL J. Biol. Chem. 266:2313-2319(1991).
 RN [3]
 RP SEQUENCE FROM N.A.

RX MEDLINE=89228054; PubMed=2712834;
 RA Sharief F.S., Lee H., Leuderman M.M., Lundwall A., Deaven L.L.,
 RA Lee C.-L., Li S.S.-L.;
 RT "Human prostatic acid phosphatase: cDNA cloning, gene mapping and
 RT protein sequence homology with lysosomal acid phosphatase";
 RL Biochem. Biophys. Res. Commun. 160:79-86(1989).
 RN [4]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Prostate;
 RX MEDLINE=88312981; PubMed=2842184;
 RA Viikio P., Viikonen P., Henttu P., Roiko K., Solin T., Huhtala M.L.;
 RT "Molecular cloning and sequence analysis of cDNA encoding human
 RT prostatic acid phosphatase";
 RL FEBS Lett. 236:275-281(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=90370491; PubMed=2395659;
 RA Tallor P.G., Govindan M.V., Patel P.C.;
 RT "Nucleotide sequence of human prostatic acid phosphatase determined
 RT from a full-length cDNA clone";
 RL Nucleic Acids Res. 18:4928-4928(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95038536; PubMed=7951074;
 RA Sharief F.S., Li S.S.-L.;
 RT "Nucleotide sequence of human prostatic acid phosphatase ACP gene,
 RT including seven Alu repeats";
 RL Biochem. Mol. Biol. Int. 33:561-565(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99023966; PubMed=9804805;
 RA Lacomte M.W., Handy G., Lebida L.;
 RT "Structural origins of L(+)-tartarate inhibition of human prostatic
 RT acid phosphatase";
 RL J. Biol. Chem. 273:30406-30409(1998).
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC DR EMBL; M97589; AAA60021.1; -;
 CC DR EMBL; M97580; AAA60021.1; JOINED.
 CC DR EMBL; M97581; AAA60021.1; JOINED.
 CC DR EMBL; M97582; AAA60021.1; JOINED.
 CC DR EMBL; M97583; AAA60021.1; JOINED.
 CC DR EMBL; M97584; AAA60021.1; JOINED.
 CC DR EMBL; M97585; AAA60021.1; JOINED.
 CC DR EMBL; M97586; AAA60021.1; JOINED.
 CC DR EMBL; M97587; AAA60021.1; JOINED.
 CC DR EMBL; M97588; AAA60021.1; JOINED.
 CC DR EMBL; M34840; AAA69694.1; -;
 CC DR EMBL; M24902; AAA60022.1; -;
 CC DR EMBL; X52174; CAA36422.1; -;
 CC DR EMBL; X53605; CAA37673.1; -;
 CC DR EMBL; U07097; AAB60640.1; -;
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 CC DR EMBL; U07085; AAB60640.1; JOINED.
 CC DR EMBL; U07086; AAB60640.1; JOINED.
 CC DR EMBL; U07088; AAB60640.1; JOINED.
 CC DR EMBL; U07091; AAB60640.1; JOINED.
 CC DR EMBL; U07092; AAB60640.1; JOINED.
 CC DR EMBL; U07093; AAB60640.1; JOINED.
 CC DR EMBL; U07095; AAB60640.1; JOINED.
 CC DR PIR; A32419; A32419.

FT	CARBONHYD	177	177	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOND	191	191	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBONHYD	267	267	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBONHYD	322	322	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBONHYD	331	331	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	423 AA;	4834 MW;	3431A30B83AE2B4	CRC64;

Query Match	49.6%	Score 1032.5	DB 1	Length 423
Best Match Similarity	51.4%	Pred. No. 9.5e-74		
Matches 189	Conservative 62	Mismatches 112	Indels 5	Gaps 3

[illegible]

```

RESULT 4
PPAL_MOUSE
ID PPAL_MOUSE STANDARD: PRT: 421 AA.
AC P24638;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LYSSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) (FRAGMENT).
GN ACP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91282986; Pubmed=2059337;
RA Geler C., von Figura K., Pohlmann R.;
RT "Molecular cloning of the mouse lysosomal acid phosphatase.";
RL Biol. Chem. Hoppe-Seyler 372:301-304(1991)
CC -1 CATALYTIC ACTIVITY: AN ORTHOPHOSPHONIC MONOESTER + H(2)O -> AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -1 SUBCELLULAR LOCATION: LYSSOMAL.
CC -1 SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
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DR	EMBL: X57199: CAA40485.1: -		
DR	PIR: S14742: S14742.		
DR	HSSP: P20646: 1RPT.		
DR	MGD: MGI:87862: ACP2.		
DR	InterPro: IPR000560: -		
DR	Pfam: pf00328: acid_phosphat; 1.		
DR	PROSITE: PS00616: HIS_ACID_PHOSPHAT_1; 1.		
DR	PROSITE: PS00778: HIS_ACID_PHOSPHAT_2; 1.		
KW	Hydrolase; Signal; Glycoprotein; Lysosome.		
FT	MONTER	1	1
FT	SIGNAL	<1	28
FT	CHAIN	29	421
FT	DISULFID	157	368
FT	DISULFID	210	308
FT	DISULFID	343	347
FT	ACT_SITE	40	40
FT	ACT_SITE	82	82
FT	ACT_SITE	284	284
FT	CARBOHYD	90	90
FT	CARBOHYD	131	131
FT	CARBOHYD	165	165
FT	CARBOHYD	175	175
FT	CARBOHYD	189	189
FT	CARBOHYD	195	195
FT	CARBOHYD	265	265
FT	CARBOHYD	320	320
FT	CARBOHYD	329	329
FT	CARBOHYD	372	372
SO	SEQUENCE	421 AA: 46279 MW: 6616431239D676D CRC64:	

Query Match	49.58;	Score 1020.5;	DB 1;	Length 421;
Best Local Similarity	51.48;	Pred. No. 1.4e-73;		
Matches 187;	Conservative 66;	Mismatches 106;	Indels 5;	Gaps 3;

[illegible]

RESULT	5		
PPAL_RAT			
ID_PPAL_RAT		STANDARD;	PRT; 423 AA.
AC	P20611:		
DT	01-EBB-1991 (Rel. 17, Created)		
DT	01-EBB-1991 (Rel. 17, Last sequence update)		
DT	01-NOV-1995 (Rel. 32, Last annotation update)		
DE	LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP).		
GN	ACP2.		

OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89350910; PubMed=2764916;
 RA Himeño M., Fujita H., Noguchi Y., Kono A., Kato K.;
 RT "Isolation and sequencing of a cDNA clone encoding acid phosphatase
 in rat liver lysosomes.";
 RL Biochem. Biophys. Res. Commun. 162:1044-1053(1989).
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M27893; AAA40744.1; -
 DR PIR: A33395; A33395.
 DR HSP: P20646; 1RPT.
 DR InterPro: IPR000560; -
 DR Pfam: PF00328; acid_phosphat; 1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolyase; Signal; Glycoprotein; Lysosome.
 FT SIGNAL 1 30
 FT CHAIN 1 423
 FT DISULFID 159 370
 FT DISULFID 212 310
 FT DISULFID 345 349
 FT ACT_SITE 42 42
 FT ACT_SITE 84 84
 FT ACT_SITE 286 286
 FT CARBOHYD 92 92
 FT CARBOHYD 133 133
 FT CARBOHYD 167 167
 FT CARBOHYD 177 177
 FT CARBOHYD 191 191
 FT CARBOHYD 197 197
 FT CARBOHYD 267 267
 FT CARBOHYD 322 322
 FT CARBOHYD 331 331
 SQ SEQUENCE 423 AA; 48319 MW; 6F4C4819CADD4496 CRC64;
 Query Match 49.5%; Score 1019.5; DB 1; Length 423;
 Best Local Similarity 51.9%; Pred. No. 1.6e-73;
 Matches 189; Conservative 61; Mismatches 109; Indels 5; Gaps 3;
 Oy 21 LLSLCL---DGGQAKELKFTVLVRRHGRGPIETFPDPTIETSSMPGQGLTOMGEBQH 77
 Db 17 LGLGCLAMPPIQARSRLEFVLLRHGRSPVAPKPDPPVQEEHMPGFGGLTKEGMLOH 76
 Oy 78 YELGSLYTRKRGFRPLNFTYKRDQIYIRSTVDFTLMSAMTALALPREGISINNPRLTW 137
 Db 77 WELGOLARQRHGFLLMSYNHGEYVASTDDFTLMSAMTALALPPTVEQHNPINISW 136
 Oy 138 QPIFVHTVSLSEDLVLPFRDCPRFEELKSETLSEEFELRLHAPKSYFLDTLSLGSFD 197
 Db 137 QPIFVHTVLPITEDRLKFRPLGRCPRYEQLOQNETROTPEYQMSIQNOQFLDMVANETGIM 196
 Oy 198 DDLFGIMSKYDPLFCESVNFPLPSATDAMIKELSELSSLSLYGCHKQKESRL 257
 Db 197 NLLETITWN-VYDPLFCFQTHGLLPPWASPOTVQALSQLDFSLFLFGTHIDVQKARL 255
 Oy 258 QGGVLYNEILKMKLALQPKYKKLYWVSANDTTVSGLOMLADVYNGVLPYASCHMMEL 317

Db 256 QGGVLLAQIILKMLTMTTSQFPLVYSADDTLVALQALNLYNKKQAPYASCHIFEL 315
 Oy 318 YHDKGHP-VEMYRNFTQNEPPLTLPGCTHSCPLEKFAELDPVLPDMATECMATSS 376
 Db 316 YQEDNGNSVEMYRNDSKAPWPLTLPGCPHRCPLDPLRTEFPVLPKDMQKCCQLASD 375
 Oy 377 HQGT 380
 Db 376 TADT 379
 RESULT 6
 ID PPAY_CAEEL STANDARD; PRT; 411 AA.
 AC Q10944;
 DT 01-NOV-1997 (Rel. 35, Created)
 DF 01-NOV-1997 (Rel. 35, Last sequence update)
 DE POTATIVE ACID PHOSPHATASE B0361.7 PRECURSOR (EC 3.1.3.2).
 GN B0361.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Du Z.;
 RL Submitted (FE8-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN
 CC -1- ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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 CC -----
 DR EMBL: U00031; AAA50626.1; -
 DR HSP: P20646; 1RPT.
 DR WormPep: B0361.7; CE00836.
 DR InterPro: IPR000560; -
 DR Pfam: PF00328; acid_phosphat; 2.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hypothetical protein; Signal; Glycoprotein; Hydrolyase.
 FT SIGNAL 1 13
 FT CHAIN 1 411
 FT ACT_SITE 40 40
 FT ACT_SITE 80 80
 FT ACT_SITE 278 278
 FT ACT_SITE 363 363
 FT DISULFID 152 302
 FT DISULFID 205 302
 FT CARBOHYD 338 342
 FT CARBOHYD 104 104
 FT CARBOHYD 210 210
 FT CARBOHYD 218 218
 FT CARBOHYD 312 312
 FT CARBOHYD 323 323
 SQ SEQUENCE 411 AA; 47110 MW; BA265D808EC8B11C CRC64;
 Query Match 26.3%; Score 542.5; DB 1; Length 411;
 Best Local Similarity 34.7%; Pred. No. 1e-35;
 Matches 135; Conservative 61; Mismatches 138; Indels 55; Gaps 14;
 Oy 19 LLSLCLD-----PGQAK--ELKFTVLVRRHGRGPIETFPDPTIETSSMPQ 64
 Db 2 LLLLVLLIGASGINAVYKKEVPIQANDTLEYVHTVWRHGRDRAELFLPDDITK--WPE 59

[illegible][illegible]

RESULT 7
PPAX CAEEL

Db 622 IDYLKPLKFYAYSSHDQLVYALLVTIGITDVVKTYDGMH

PD TSSSLTIEYYSNPGNQSSVK 681

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RESULT      9
PPRV_CABEEL
ID PPRV_CABEEL STANDARD; PRT; 471 AA.
AC 009448;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE ACID PHOSPHATASE C05C10.1 (EC 3.1.3.2) (FRAGMENT).
GN C05C10.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Matthews P.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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RESULT	10			
AGR_ECOLI				
ID	AGR_ECOLI	STANDARD:	PRT:	413 AA.
AC	P19926;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	GLUCOSE-1-PHOSPHATASE PRECURSOR (EC 3.1.3.10) (G1PASE).			
CN	AGP.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
RM	[1]			
RM	SEQUENCE FROM N.A., AND SEQUENCE OF 23-31.			
RP	STRAIN-K12;			
RC	MEDLINE=90130318; PubMed=2153660;			
RX	Pridel E., Marck C., Boquet P. L.;			
RA	"Nucleotide sequence and transcriptional analysis of the Escherichia			
RT	coli agp gene encoding periplasmic acid glucose-1-phosphatase.";			


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QY 10 PTLISLGFLLLSLCLDPCQAKLKFVTLVFRNGDGRPIETE---PTDPTSSSQGF 66
Db 350 PVTSLPHSTLWVMCI-----QMKYVDY-FLDELIDTLLEKGDPIETETE--- 398
QY 67 GOLTQMGEOHQEYELGASYIRKRYG-----RFLND--TYKHQOIVRSTDVDRTLTSM 116
Db 399 ---TTRW-YNNHNDITILYIKRYGCPMMKRMKEIYELTREAASHLLKTDENRG--- 450
QY 117 TNLALFPPPGIS----TWNPLLMOPIPV---HTVSLSEDRLLYLPFRDCPFEE 165
Db 451 ---AIMEFPPTICLPYLLCCNMYKLKQIPFKEENRNIIYKKKNRVL-----C-FDS 499
QY 166 LKSFTESEEFKRLHMYKSFLOTLSLSGDDODDLGIMSXYDPLFC-----ESVH 219
Db 500 LENAEPF-----LKIIDSIPGLKTYNMMDIYENSNNITCVAFIPQESIH 546
QY 220 FTLSPMATEDAMIKLKESELSTSLXGHHOKERSKLOGVLVNETLKMKLATOPQY 279
Db 547 -----EERKRL-QLFDIARLASGLVIIPSRYLSSMTPVYNNM--EGRETTNQKI 595
QY 280 KKLV---MYSAH-----DTVSGLOMALDYVNGVLPY---ASCNME 316
Db 596 ECLVILLDFSEEFLEYONIGNAVSNKYELETYISNYOALINCLMSTLLIYLGSIIRSIS 655
QY 317 LYHDKGHVEVMYR---NQTONEP 338
Db 656 KTEDFVUSILNIEFYKGLKINILLSEP 681

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RESULT	12			
VE02_VACCV				
ID	VE02_VACCV	STANDARD:	PRT:	737 AA.
AC	p21604;			
DT	01-MAY-1991 (Rel. 18, Created)			
PT	01-NOV-1991 (Rel. 20, Last sequence update)			
DE	01-NOV-1991 (Rel. 20, Last annotation update)			
GN	PROTEIN E2.			
OS	E2L.			
OC	Vaccinia virus (strain WR).			
OC	viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
OX	NCBI_TaxID=10254;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA	Gershon P.D., Jones E.V., Moss B., Ahn B.-Y.;			
RL	submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 1-597 FROM N.A.			
RX	MEDLINE=90377234; PubMed=2398897;			
RA	Ahn B.-Y., Gershon P.D., Jones E.V., Moss B.;			
RT	"Identification of rpo30, a vaccinia virus RNA polymerase gene with			
RT	structural similarity to a eucaryotic transcription elongation			
RT	factor.";			
RL	Mol. Cell. Biol. 10:5433-5441(1990).			
CC	-----			
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CC	-----			
DR	EMBL; M36339; AAB59822.1; -			
DR	PIR; A35928; A35928.			
SQ	SEQUENCE 737 AA; 85957 MW; D5BAF09E2F944A9E CRC64;			
Query Match	5.4%;	Score 110.5;	DB 1;	Length 737;
Best Local Similarity	21.2%;	Pred. No. 0.37;		
Matches 82;	Conservative 68;	Mismatches 125;	Indels 111;	Gaps 21;
10	PTASISGAEFLLLSLCDPGAAKELKVTYLVFRHGRPIETFE---PNDPTTESSWPGGF	66		

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Db 350 PVTSLPHISTVLWMCJ-----OMKYVDY-ERLDEIDIDTLIEKADPTTETTF-----398H
QY 67 GOLTOMGEHOEYELGSYIRKRYG-----RFLND---TYKHQDIYTRSDVDVTRLTMSAM 116Q
Db 399 ---TRW-YNKINDILITLYIKRYGCPMMKRLMEFYLPTEASDHLKLTNDENRG-----450D
QY 117 TNLALPPEPES-----INPRLWQPIPV-----HTVSLSEDRLLYLPFRDCPREE 165Q
Db 451 ---AIMFEPRICTLPYLCCNYKLIKQPIPEKRENNIYKKNNRVL-----C-FDS 499D
QY 166 LKSETSESEELKRLHPKPSLDTLUSLSGFDODLFGIMSKYVDPLFC-----ESVHN 219Q
Db 500 LENSASFCS-----LIKIDSIPLGLKTYNMMDIYEKSNITICVAFIPOSEIHN 546D
QY 220 FTLPDMATEDMILKELSELSSLISLYGIHKQKRSKRLQSGVLVNEILKMKMLTPOQY 279Q
Db 547 -----EERRIKL-QLFDIARLASGYLYIPSRYSLSWTPVNMJ--EGRETYNOKI 595D
QY 280 KKLIV---MYSAH-----DTTYSGLQMALDVNYGVLPPY---ASCHMME 316Q
Db 596 ECLVILDLFSEEFLEYONMGNAVSNKRYELETTYSIYQAINCMJSTLLIYVLGSIIRSIS 655D
QY 317 LYHDGCGHFVEMYR---NETONEP 338Q
Db 656 RTENFVLSILNIWIFYKGLKINLELSEP 681D

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RESULT	13				
ID	RRPO_PEAMV	STANDARD;	PRT;	599	AA.
AC	P29154;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48).				
OS	Pea enation mosaic virus (PEMV).				
OC	viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;				
OC	Enamovirus.				
OX	NCBI_TaxID=12290;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MSG:				
RX	MEDLINE=91341468; PubMed=1875194;				
RA	Demler S.A., de Zoeten G.A.;				
RT	"The nucleotide sequence and luteovirus-like nature of RNA 1 of an				
RT	aphid non-transmissible strain of pea enation mosaic virus.";				
RL	J. Gen. Virol. 72:1819-1834(1991).				
CC	-1- SIMILARITY: TO LUTEOVIRUS RNA-DIRECTED RNA POLYMERASES.				
CC	-----				
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CC	-----				
CC	EMBL; L04573; AAA72297.1; ALT_INIT.				
DR	InterPro: IPR00195;				
DR	Pfam: PF02123; Luteo_ORF3; 1.				
DR	PRINTS: PR00914; LVTRUSRNAPOL.				
KW	Transferase; RNA-directed RNA polymerase.				
FT	VARIA NT	66	66	G -> S.	
FT	VARIA NT	78	78	Q -> P.	
FT	VARIA NT	84	84	S -> I.	
FT	VARIA NT	93	93	T -> I.	
FT	VARIA NT	95	95	R -> G.	
FT	VARIA NT	104	104	R -> H.	
FT	VARIA NT	336	336	V -> L.	
FT	VARIA NT	359	359	I -> K.	
FT	VARIA NT	410	410	S -> F.	

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